

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 27, 2001, 14:49:08 ; Search time 1726.63 Seconds
(without alignments)
11207.492 Million cell updates/sec

Title: US-09-435-054-1
Perfect score: 1173
Sequence: 1 ccacgctccgccaccacac.....tcaaaaaaaaaaaaaaaaaa 1173

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1472140 seqs, 8248589755 residues

Word size : 10

Total number of hits satisfying chosen parameters: 1091308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl:

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.om.*
- 20: em.or.*
- 21: em.ov.*
- 22: em.pat.*
- 23: em.ph.*
- 24: em.pl.*
- 25: em.ro.*
- 26: em.sts.*
- 27: em.sy.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htgo_hum.*
- 31: em.htgo_inv.*
- 32: em.htgo_rod.*
- 33: em.htg_hum.*
- 34: em.htg_inv.*
- 35: em.htg_rod.*
- 36: em.htg_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	30	2.6	214005	2	AC064803	Mus muscu
C 2	29	2.5	185996	2	AC041023	AC041023 Homo sapi
C 3	26	2.2	602	8	LES133600	AD133600 Lycopersi
C 4	26	2.2	2518	3	AF309947	AF309947 Dictyoste
C 5	26	2.2	2580	3	AF145620	AF145620 Drosophil
C 6	26	2.2	5575	9	HSM802758	AL390127 Homo sapi
C 7	26	2.2	110000	2	PFMAL4PL_0	AC034557 Plasmodiu
C 8	26	2.2	163443	2	AC006280	AC006280 Plasmodiu
C 9	26	2.2	207596	2	AL590630	AL590630 Mus muscu
C 10	25	2.1	1318	8	NTUPGENE	Y11210 N tabacum m
C 11	25	2.1	1445	5	GK606GENE	Y14971 Gallus gall
C 12	25	2.1	1498	3	CE19144	Y19144 Ceratitiss c
C 13	25	2.1	1572	3	COA19145	Y19145 Ceratitiss c
C 14	25	2.1	1633	9	AK026358	AK026358 Homo sapi
C 15	25	2.1	1683	3	AF057693	AF057693 Sacculina
C 16	25	2.1	1705	3	DDU20806	U20806 Dictyostelli
C 17	25	2.1	1891	3	OVI15993	Y15993 Onchocerca
C 18	25	2.1	2691	5	XL059483	U59483 xenopus lae
C 19	25	2.1	2703	5	XL089707	U89707 xenopus lae
C 20	25	2.1	2771	3	AF083225	AF083225 Caenorhab
C 21	25	2.1	3268	3	PFRESAG1	X04572 P.falciparu
C 22	25	2.1	4591	6	A00661	A00661 P.falciparu
C 23	25	2.1	20413	9	AC004631	AC004631 Homo sapi
C 24	25	2.1	25147	2	AC014449	AC014449 Drosophil
C 25	25	2.1	34000	9	AC006540	AC006540 Homo sapi
C 26	25	2.1	43324	2	AC034287	AC034287 Mus muscu
C 27	25	2.1	47827	8	AP000731	AP000731 Arabidops
C 28	25	2.1	57698	9	HSJ753M9	AL079301 Human DNA
C 29	25	2.1	63331	2	AC084345	AC084345 Homo sapi
C 30	25	2.1	73880	2	AC090728	AC090728 Homo sapi
C 31	25	2.1	81447	2	AC034306	AC034306 Homo sapi
C 32	25	2.1	83948	8	AB012246	AB012246 Arabidops
C 33	25	2.1	85812	2	AC040952	AC040952 Homo sapi
C 34	25	2.1	86677	2	AC005646	AC005646 Drosophil
C 35	25	2.1	86827	3	PFMAL3P5	AL034556 Plasmodiu
C 36	25	2.1	87400	8	AC010796	AC010796 Arabidops
C 37	25	2.1	95477	9	AC007076	AC007076 Homo sapi
C 38	25	2.1	101157	9	AL356791	AL356791 Human DNA
C 39	25	2.1	128266	9	AC008623	AC008623 Homo sapi
C 40	25	2.1	131541	2	AC006594	AC006594 Homo sapi
C 41	25	2.1	135056	9	AL445071	AL445071 Human DNA
C 42	25	2.1	142339	8	AF003266	AF003266 Oryza sat
C 43	25	2.1	144075	2	AC013763	AC013763 Homo sapi
C 44	25	2.1	146574	2	AC023459	AC023459 Homo sapi
C 45	25	2.1	147246	2	AC023196	AC023196 Homo sapi
C 46	25	2.1	149008	9	AC007991	AC007991 Homo sapi
C 47	25	2.1	152409	2	PFMAL1P1	AL031744 Plasmodiu
C 48	25	2.1	153846	2	AC023252	AC023252 Homo sapi
C 49	25	2.1	156847	33	AC073662	AC073662 Homo sapi
C 50	25	2.1	157525	2	AC083838	AC083838 Homo sapi
C 51	25	2.1	157747	2	AL158834	AL158834 Homo sapi
C 52	25	2.1	159468	2	AC015280	AC015280 Drosophil
C 53	25	2.1	160209	9	AC012324	AC012324 Homo sapi
C 54	25	2.1	160903	3	AC007580	AC007580 Drosophil
C 55	25	2.1	162908	2	AC046195	AC046195 Homo sapi
C 56	25	2.1	163345	2	AL360002	AL360002 Homo sapi
C 57	25	2.1	165106	2	AC016034	AC016034 Homo sapi
C 58	25	2.1	165868	9	AC010651	AC010651 Homo sapi
C 59	25	2.1	166076	2	AC090587	AC090587 Homo sapi
C 60	25	2.1	169103	2	AC025687	AC025687 Homo sapi
C 61	25	2.1	169210	2	AC055641	AC055641 Homo sapi
C 62	25	2.1	169689	3	AC008306	AC008306 Drosophil
C 63	25	2.1	170282	3	AC006467	AC006467 Drosophil
C 64	25	2.1	171805	9	AC020716	AC020716 Homo sapi
C 65	25	2.1	173760	9	AL354653	AL354653 Human DNA
C 66	25	2.1	174084	2	AC090695	AC090695 Homo sapi
C 67	25	2.1	174551	9	AC010598	AC010598 Homo sapi
C 68	25	2.1	175872	33	AC011878	AC011878 Homo sapi
C 69	25	2.1	175952	2	AC012060	AC012060 Homo sapi
C 70	25	2.1	176278	2	AC091305	AC091305 Homo sapi

71	25	2.1	177309	2	AL592226	AL592226 Homo sapi	144	24	2.0	95870	8	AC026757	AC026757 Arabidops
72	25	2.1	178035	2	AC068680	AC068680 Homo sapi	145	24	2.0	96299	9	AL133519	AL133519 Human DNA
73	25	2.1	179550	2	AL603626	AL603626 Homo sapi	146	24	2.0	97684	9	HS0309122	HS0309122 Homo sapi
74	25	2.1	179936	2	AC025491	AC025491 Homo sapi	147	24	2.0	100000	9	AP0000084	AP0000084 Homo sapi
75	25	2.1	180551	2	AC004158	AC004158 Homo sapi	148	24	2.0	100000	9	AP000136	AP000136 Homo sapi
76	25	2.1	181006	2	AC020780	AC020780 Homo sapi	149	24	2.0	107554	2	AC084697	AC084697 Homo sapi
77	25	2.1	181166	2	AC025251	AC025251 Homo sapi	150	24	2.0	109173	9	AC007678	AC007678 Homo sapi
78	25	2.1	181636	2	AC025108	AC025108 Homo sapi	151	24	2.0	109612	9	AL512503	AL512503 Human DNA
79	25	2.1	183560	2	AP003063	AP003063 Homo sapi	152	24	2.0	110000	2	AC046137_3	Continuation (3 of
80	25	2.1	183892	2	AC092977	AC092977 Homo sapi	153	24	2.0	110000	2	AL354792_2	Continuation (4 of
81	25	2.1	183918	2	AC025896	AC025896 Homo sapi	154	24	2.0	110015	2	AL450323	Continuation (3 of
82	25	2.1	185764	2	AC025289	AC025289 Homo sapi	155	24	2.0	111694	9	HSJ3836N17	AL450323 Mus muscu
83	25	2.1	191674	2	AC022975	AC022975 Homo sapi	156	24	2.0	115995	9	AC011494	AL049539 Human DNA
84	25	2.1	196725	2	AC055873	AC055873 Homo sapi	157	24	2.0	116524	9	AL138686	AL011494 Homo sapi
85	25	2.1	197872	2	AC037476	AC037476 Homo sapi	158	24	2.0	117616	2	AC091249	AL138686 Human DNA
86	25	2.1	199551	2	AC006281	AC006281 Plasmodi	159	24	2.0	118492	2	AC020548	AC091249 Mus muscu
87	25	2.1	201327	2	AL591709	AL591709 Homo sapi	160	24	2.0	119456	2	AC084789	AC020548 Homo sapi
88	25	2.1	201874	2	AC026472	AC026472 Homo sapi	161	24	2.0	119484	9	AC005064	AC084789 Homo sapi
89	25	2.1	205429	2	AC005506	AC005506 Plasmodi	162	24	2.0	120433	2	AC092287	AC005064 Homo sapi
90	25	2.1	212658	2	AC068868	AC068868 Homo sapi	163	24	2.0	121245	2	AC034240	AC092287 Homo sapi
91	25	2.1	260713	3	AE003814	AE003814 Drosophil	164	24	2.0	122056	9	AF283320S1	AC034240 Homo sapi
92	25	2.1	293431	2	PFMAL13P4	AL049181 Plasmodi	165	24	2.0	122302	9	AC003982	AF283320 Homo sapi
93	25	2.1	298283	3	AE003782	AE003782 Drosophil	166	24	2.0	122742	9	HS167P19	AC003982 Homo sapi
94	25	2.1	321003	2	PFMAL4P3	AL035476 Plasmodi	167	24	2.0	124048	9	HUAC002045	293014 Homo sapien
95	24	2.0	542	8	AF336985	AF336985 Plasmodi	168	24	2.0	131329	2	AL354887	AC002045 Human Chr
96	24	2.0	666	8	CAR7556	AJ007556 Cicer ari	169	24	2.0	135276	2	AC073603	AL354887 Homo sapi
97	24	2.0	837	8	AF015785	AF015785 Phaseolus	170	24	2.0	135369	2	AC090557	AC073603 Mus muscu
98	24	2.0	886	6	AR123127	AR123127 Sequence	171	24	2.0	135552	9	AL019251	AC090557 Homo sapi
99	24	2.0	886	6	AR124079	AR124079 Sequence	172	24	2.0	138347	9	AL389889	AL019251 Homo sapi
100	24	2.0	886	6	AF243376	AF243376 Glycine m	173	24	2.0	143427	9	AC002432	AL389889 Human DNA
101	24	2.0	937	5	CCA308993	AF308993 Cyprinus	174	24	2.0	143804	2	AC012617	AC002432 Human BAC
102	24	2.0	1030	8	AF003728	AF003728 Arabidops	175	24	2.0	144449	2	AC067926	AC012617 Homo sapi
103	24	2.0	1210	9	BC009956	BC009956 Homo sapi	176	24	2.0	144694	2	AC011321	AC067926 Mus muscu
104	24	2.0	1372	9	AF144755	AF144755 Homo sapi	177	24	2.0	144877	2	AL157408	AC011321 Homo sapi
105	24	2.0	1431	9	BC000409	BC000409 Homo sapi	178	24	2.0	145988	2	AC024059	AL157408 Homo sapi
106	24	2.0	1466	6	AX105363	AX105363 Sequence	179	24	2.0	146006	9	AC005103	AC024059 Homo sapi
107	24	2.0	1520	9	BC009376	BC009376 Homo sapi	180	24	2.0	146006	9	AC005103	AC005103 Homo sapi
108	24	2.0	1552	8	AF246715	AF246715 Phalaenop	181	24	2.0	146460	33	AC007913	AC005103 Homo sapi
109	24	2.0	1606	3	DDU41222	U41222 Dictyosteli	182	24	2.0	147327	2	AC078905	AC007913 Homo sapi
110	24	2.0	1890	9	AB051123	AB051123 Macaca fa	183	24	2.0	147386	2	AC092065	AC078905 Homo sapi
111	24	2.0	1928	6	AX192162	AX192162 Sequence	184	24	2.0	147621	2	AC060763	AC092065 Homo sapi
112	24	2.0	2031	9	BC000964	BC000964 Homo sapi	185	24	2.0	147708	9	HS179M20	AC060763 Homo sapi
113	24	2.0	2040	9	BC007746	BC007746 Homo sapi	186	24	2.0	147889	2	AC018534	297053 Human DNA s
114	24	2.0	2210	9	AB056838	AB056838 Macaca fa	187	24	2.0	148260	2	AL596222	AL018534 Homo sapi
115	24	2.0	2214	8	MTR310820	AJ310820 Medicago	188	24	2.0	149542	9	AC011711	AL596222 Homo sapi
116	24	2.0	2259	9	AC025591	AC025591 Homo sapi	189	24	2.0	150150	2	AC022003	AC011711 Homo sapi
117	24	2.0	2307	8	MSA311050	AJ311050 Medicago	190	24	2.0	150959	2	AC019250	AC022003 Homo sapi
118	24	2.0	2327	6	AR087435	AR087435 Sequence	191	24	2.0	150959	2	AC019250	AC019250 Homo sapi
119	24	2.0	2858	10	BC003239	BC003239 Mus muscu	192	24	2.0	151479	2	AC012278	AC019250 Homo sapi
120	24	2.0	2993	6	AR071756	AR071756 Sequence	193	24	2.0	151964	9	AF047825	AC012278 Homo sapi
121	24	2.0	3000	9	AK026673	AK026673 Homo sapi	194	24	2.0	151964	9	AF047825	AF047825 Homo sapi
122	24	2.0	3114	3	DVI249251	AJ249251 Drosophil	195	24	2.0	152450	2	AC090141	AF047825 Homo sapi
123	24	2.0	3601	9	HSN801924	AL137651 Homo sapi	196	24	2.0	152450	2	AC090141	AC090141 Homo sapi
124	24	2.0	3997	9	AK025513	AK025513 Homo sapi	197	24	2.0	152499	2	AC032008	AC090141 Homo sapi
125	24	2.0	7236	3	AF310890	AF310890 Dictyoste	198	24	2.0	154312	2	AC011492	AC032008 Homo sapi
126	24	2.0	7622	3	AF112367	AF112367 Plasmodi	199	24	2.0	154467	2	AC022566	AC011492 Homo sapi
127	24	2.0	13684	3	AE001403	AE001403 Plasmodi	200	24	2.0	155139	2	AL590436	AC022566 Homo sapi
128	24	2.0	14613	3	AE001396	AE001396 Plasmodi	201	24	2.0	155621	2	AL590436	AL590436 Homo sapi
129	24	2.0	15861	3	AE001413	AE001413 Plasmodi	202	24	2.0	156510	2	AL356976	AL590436 Homo sapi
130	24	2.0	3522	9	AC068948	AC068948 Homo sapi	203	24	2.0	156549	2	AC079072	AL356976 Homo sapi
131	24	2.0	41924	2	AC087403	AC087403 Homo sapi	204	24	2.0	156571	2	AC027431	AC079072 Homo sapi
132	24	2.0	43241	9	HSJ9613	AJ009613 Homo sapi	205	24	2.0	157436	2	AC025682	AC027431 Homo sapi
133	24	2.0	45397	2	AC010417	AC010417 Homo sapi	206	24	2.0	157579	2	AC011152	AC025682 Homo sapi
134	24	2.0	48563	2	AC092824	AC092824 Homo sapi	207	24	2.0	158431	9	AC008115	AC011152 Homo sapi
135	24	2.0	61013	2	AC090456	AC090456 Homo sapi	208	24	2.0	160114	2	AC023073	AC008115 Homo sapi
136	24	2.0	61209	9	AP000220	AP000220 Homo sapi	209	24	2.0	160979	2	AC055879	AC023073 Homo sapi
137	24	2.0	71306	9	AC007423	AC007423 Homo sapi	210	24	2.0	161164	2	AC022278	AC055879 Homo sapi
138	24	2.0	71196	2	AL590419_3	Continuation (4 of	211	24	2.0	161428	2	AC022679	AC022278 Homo sapi
139	24	2.0	73395	9	AC008848	AL356742 Human DNA	212	24	2.0	161692	2	AC090179	AC022679 Homo sapi
140	24	2.0	75588	9	AL356742	AL356742 Human DNA	213	24	2.0	162452	2	AC069239	AC090179 Homo sapi
141	24	2.0	79779	9	HSJ710H13	AL121712 Human DNA	214	24	2.0	162573	9	CNS00M8L	AC069239 Homo sapi
142	24	2.0	83844	2	AC008708	AC008708 Homo sapi	215	24	2.0	162959	2	AC019255	AL079304 Human Chr
143	24	2.0	95173	8	AC068324	AC068324 Arabidops	216	24	2.0	163871	9	HS1158E12	AC019255 Homo sapi

217	24	2.0	164471	2	AC069500	Homo sapi
218	24	2.0	164584	2	AC021469	Homo sapi
219	24	2.0	164975	2	AC092702	Homo sapi
220	24	2.0	165077	2	AC024493	Homo sapi
221	24	2.0	165077	2	AC024493	Homo sapi
222	24	2.0	165600	2	AC097980	Homo sapi
223	24	2.0	166053	2	AC091559	Homo sapi
224	24	2.0	166332	2	AC068955	Homo sapi
225	24	2.0	167294	2	AC013814	Homo sapi
226	24	2.0	168384	2	AC068774	Homo sapi
227	24	2.0	168799	9	AC009531	Homo sapi
228	24	2.0	168872	9	AC073325	Homo sapi
229	24	2.0	168880	9	AC073325	Homo sapi
230	24	2.0	169546	2	AC004157	Plasmodiu
231	24	2.0	169647	2	AC025343	Homo sapi
232	24	2.0	169851	2	AL592211	Homo sapi
233	24	2.0	170118	9	AC012384	Homo sapi
234	24	2.0	170389	2	AC016225	Homo sapi
235	24	2.0	170394	2	AC024371	Homo sapi
236	24	2.0	170473	2	AC021523	Homo sapi
237	24	2.0	170814	2	AC021686	Homo sapi
238	24	2.0	171304	2	AC090297	Homo sapi
239	24	2.0	171757	9	CNS01080	Human chr
240	24	2.0	171965	2	AC027507	Homo sapi
241	24	2.0	172033	2	AC008949	Homo sapi
242	24	2.0	172757	2	AL591848	Homo sapi
243	24	2.0	173310	2	AC090454	Homo sapi
244	24	2.0	173801	2	AC022257	Homo sapi
245	24	2.0	173825	2	AC011037	Homo sapi
246	24	2.0	174147	9	AC018891	Homo sapi
247	24	2.0	174642	2	AC091769	Homo sapi
248	24	2.0	175684	2	AC073343	Homo sapi
249	24	2.0	176226	2	AC026583	Homo sapi
250	24	2.0	176806	2	AC090438	Homo sapi
251	24	2.0	176976	2	AC012213	Homo sapi
252	24	2.0	177263	2	AC079775	Homo sapi
253	24	2.0	177444	2	AC084238	Mus muscu
254	24	2.0	178089	2	AC093133	Papio cyn
255	24	2.0	178252	2	AC023933	Homo sapi
256	24	2.0	179428	2	AC068531	Homo sapi
257	24	2.0	179780	2	AC021013	Homo sapi
258	24	2.0	180676	2	AC022080	Homo sapi
259	24	2.0	180836	2	AC025241	Homo sapi
260	24	2.0	181413	2	AC023818	Homo sapi
261	24	2.0	181712	2	AF001103	Homo sapi
262	24	2.0	181923	9	AC022872	Homo sapi
263	24	2.0	181991	2	AC068322	Homo sapi
264	24	2.0	182641	2	AC008021	Homo sapi
265	24	2.0	183414	2	AC024188	Homo sapi
266	24	2.0	184643	2	AC087650	Homo sapi
267	24	2.0	184831	2	AC016030	Homo sapi
268	24	2.0	185939	2	AL451007	Homo sapi
269	24	2.0	186406	2	AC087828	Homo sapi
270	24	2.0	186785	9	AC010267	Homo sapi
271	24	2.0	187009	2	AC061710	Homo sapi
272	24	2.0	187292	2	AC061711	Homo sapi
273	24	2.0	189126	2	AC016670	Homo sapi
274	24	2.0	189245	2	AC018466	Homo sapi
275	24	2.0	189570	2	AC019120	Homo sapi
276	24	2.0	189791	2	AC011629	Homo sapi
277	24	2.0	190815	9	AC007066	Homo sapi
278	24	2.0	190950	2	AL359639	Homo sapi
279	24	2.0	191312	2	AF001030	Homo sapi
280	24	2.0	192929	2	AC005505	Plasmodiu
281	24	2.0	194391	2	AC091245	Homo sapi
282	24	2.0	194841	2	AC021139	Homo sapi
283	24	2.0	196841	2	AC018901	Homo sapi
284	24	2.0	196900	2	AC074366	Homo sapi
285	24	2.0	196930	2	AL359758	Homo sapi
286	24	2.0	197103	2	AC027544	Homo sapi
287	24	2.0	197278	2	AF001850	Homo sapi
288	24	2.0	197639	2	AL365504	Homo sapi
289	24	2.0	197844	2	AC079176	Homo sapi
290	24	2.0	199016	2	AC021387	Homo sapi
291	24	2.0	199600	2	AC005528	Mus muscu
292	24	2.0	200000	2	AC008076	Homo sapi
293	24	2.0	200168	9	AC008760	Homo sapi
294	24	2.0	201804	2	AC091754	Papio cyn
295	24	2.0	203420	2	AC074207	Mus muscu
296	24	2.0	204407	2	AC090443	Mus muscu
297	24	2.0	204703	2	AC092698	Homo sapi
298	24	2.0	206281	2	AL160282	Homo sapi
299	24	2.0	208172	2	AC093164	Homo sapi
300	24	2.0	210359	9	HS4430K20	Human DNA
301	24	2.0	211039	2	AC068555	Homo sapi
302	24	2.0	213973	2	AC083948	Mus muscu
303	24	2.0	215164	2	AL136368	Homo sapi
304	24	2.0	215260	2	AC073796	Mus muscu
305	24	2.0	218195	2	AC009600	Homo sapi
306	24	2.0	218829	2	AC078926	Homo sapi
307	24	2.0	228364	2	AC027243	Homo sapi
308	24	2.0	237653	2	AL593847	Mus muscu
309	24	2.0	300503	2	AC073760	Mus muscu
310	24	2.0	310779	2	AC010260	Homo sapi
311	24	2.0	340000	9	AP001693	Plasmodiu
312	24	2.0	42	6	AF020971	Homo sapi
313	23	2.0	42	6	AR043386	Sequence
314	23	2.0	42	6	AR062301	Sequence
315	23	2.0	48	6	AR020989	Sequence
316	23	2.0	48	6	AR043404	Sequence
317	23	2.0	48	6	AR062319	Sequence
318	23	2.0	312	9	HS184XG5	H. sapiens
319	23	2.0	314	5	AF266226	Gillichth
320	23	2.0	396	6	AX093212	Sequence
321	23	2.0	401	6	AX072085	Sequence
322	23	2.0	478	3	AF352722	Cooperia
323	23	2.0	572	9	HST000258	Homo sapi
324	23	2.0	615	9	HSFALL39	H. sapiens m
325	23	2.0	634	9	HSCAP18PN	H. sapiens m
326	23	2.0	671	9	BC012164	Homo sapi
327	23	2.0	671	9	BC007606	Homo sapi
328	23	2.0	714	3	AB038152	Dictyoste
329	23	2.0	750	9	HST000256	Homo sapi
330	23	2.0	753	9	HSB002224	Homo sapi
331	23	2.0	760	6	AX003614	Sequence
332	23	2.0	790	9	AF339770	Homo sapi
333	23	2.0	812	10	AB039823	Rattus no
334	23	2.0	819	8	LAU89841	Lupinus ang
335	23	2.0	835	9	AK024767	Homo sapi
336	23	2.0	854	9	BC005921	Homo sapi
337	23	2.0	906	6	AX156357	Sequence
338	23	2.0	907	10	CPDPPPKI	C. porcellus
339	23	2.0	991	10	CPGPPPKI	C. porcellus
340	23	2.0	991	8	AF336285	Gossypium
341	23	2.0	1005	9	HOM6PSG1	Homo sapi
342	23	2.0	1005	9	BC002819	Homo sapi
343	23	2.0	1006	10	CPBPPTKI	C. porcellus
344	23	2.0	1014	9	BC008418	Homo sapi
345	23	2.0	1036	6	AR103418	Sequence
346	23	2.0	1056	10	AF038848	Mus muscu
347	23	2.0	1079	8	AY045976	Arabidops
348	23	2.0	1082	3	DDU06453	Dictyosteli
349	23	2.0	1106	8	AF093616	Acetabula
350	23	2.0	1140	3	SCMEGGANT	Schistosoma
351	23	2.0	1166	10	BC003454	Mus muscu
352	23	2.0	1168	10	MMICAM2	X65493 M. musculus
353	23	2.0	1223	8	THCHIT33	X80006 T. harzianum
354	23	2.0	1239	10	AF000577	Rattus no
355	23	2.0	1244	8	ATSEB2	Y14424 Arabidops
356	23	2.0	1246	9	HSV526F1B	270282 Human DNA s
357	23	2.0	1261	9	HST000208	AL079294 Homo sapi
358	23	2.0	1279	9	BC002125	Mus muscu
359	23	2.0	1280	9	BC000491	BC002125 Homo sapi
360	23	2.0	1282	9	BC000504	BC000491 Homo sapi
361	23	2.0	1300	9	BC000794	BC000504 Homo sapi
362	23	2.0	1301	9	HSB802748	AL359939 Homo sapi

363	23	2.0	1310	3	AF202634	AF202634 Drosophil	436	23	2.0	2495	6	A83552	A83552 Sequence 1
364	23	2.0	1314	5	CCQPD10	Y14631 Cyprin ca	437	23	2.0	2495	8	NTCHLDMC	Y10022 N. tabacum m
365	23	2.0	1359	4	AF020510	AF020510 Bos tauri	438	23	2.0	2508	10	BC006674	BC006674 Mus muscu
366	23	2.0	1382	3	AF317731	AF317731 Schistos	439	23	2.0	2568	3	DDP8A7	X51947 Dictyostell
367	23	2.0	1412	9	S78159	S78159 Homo sapien	440	23	2.0	2582	3	AK025715	AK025715 Homo sapi
368	23	2.0	1414	9	AF131847	AF131847 Homo sapi	441	23	2.0	2591	8	AF036873	AF036873 Phaneroch
369	23	2.0	1451	3	AF201906	AF201906 Drosophil	442	23	2.0	2672	9	HSCSEIG7	AF036873 Homo sapi
370	23	2.0	1452	3	AF380366	AF380366 Schistos	443	23	2.0	2678	5	AF016244	AF016244 Homo sapi
371	23	2.0	1453	9	AK000191	AK000191 Homo sapi	444	23	2.0	2680	9	BC002549	BC002549 Homo sapi
372	23	2.0	1502	5	AF132247	AF132247 Dario rer	445	23	2.0	2722	9	BC007319	BC007319 Homo sapi
373	23	2.0	1506	22	E09126	E09126 cDNA encodi	446	23	2.0	2745	9	AF064087	AF064087 Homo sapi
374	23	2.0	1532	6	AX000692	AX000692 Sequence	447	23	2.0	2751	9	HSU80191	HSU80191 Human TFIID
375	23	2.0	1534	9	HSU801279	AL122116 Homo sapi	448	23	2.0	2754	9	AF062537	AF062537 Homo sapi
376	23	2.0	1535	8	NPV08292	Y08292 N. plumbagin	449	23	2.0	2886	3	HSU802641	AL355936 Homo sapi
377	23	2.0	1545	9	AK000609	AK000609 Homo sapi	450	23	2.0	2896	3	CEL277649	AJ277649 Caenorhab
378	23	2.0	1548	9	BC000784	BC000784 Homo sapi	451	23	2.0	2946	3	BC005140	BC005140 Homo sapi
379	23	2.0	1559	10	MM007635	U07635 Mus musculu	452	23	2.0	2985	3	DDU31631	U31631 Dictyostell
380	23	2.0	1582	9	BC005946	BC005946 Homo sapi	453	23	2.0	3015	3	BC003138	BC003138 Homo sapi
381	23	2.0	1597	8	AF338237	AF338237 Zantedesc	454	23	2.0	3073	9	BC003138	BC003138 Homo sapi
382	23	2.0	1662	9	BC008718	BC008718 Homo sapi	455	23	2.0	3080	4	DOGFIKA	AL137446 Homo sapi
383	23	2.0	1671	3	AF140780	AF140780 Dictyoste	456	23	2.0	3109	9	HSU802156	AK000054 Homo sapi
384	23	2.0	1686	8	SOL250433	AJ250433 Spinacia	457	23	2.0	3229	9	AK000054	AK000054 Dictyoste
385	23	2.0	1689	9	HSU802149	AL137697 Homo sapi	458	23	2.0	3292	3	AF300334	AF300334 Dictyoste
386	23	2.0	1708	3	TRC223614	AJ223614 Tribolium	459	23	2.0	3392	9	HSU800879	AF283323 Caenorhab
387	23	2.0	1731	8	AY035141	AY035141 Arabidops	460	23	2.0	3460	3	AF283323	AF283323 Caenorhab
388	23	2.0	1749	10	AF084568	AF084568 Mesocrice	461	23	2.0	3701	3	AF283322	AF283322 Caenorhab
389	23	2.0	1750	10	AF084569	AF084569 Mesocrice	462	23	2.0	3833	9	AF399910	AF399910 Homo sapi
390	23	2.0	1752	9	BC002642	BC002642 Homo sapi	463	23	2.0	4000	8	ZMA250986	AJ250986 Zea mays
391	23	2.0	1755	9	AF052099	AF052099 Homo sapi	464	23	2.0	4205	6	AF035940	AF035940 Sequence
392	23	2.0	1779	9	AK026307	AK026307 Homo sapi	465	23	2.0	4205	6	AF084558	AF084558 Homo sapi
393	23	2.0	1782	9	BC002936	BC002936 Homo sapi	466	23	2.0	4205	6	AF310896	AF310896 Dictyoste
394	23	2.0	1791	8	ATALLXSN	X92510 A. thaliana	467	23	2.0	4596	3	AF310896	AF310896 Dictyoste
395	23	2.0	1796	9	BC007064	BC007064 Homo sapi	468	23	2.0	4764	9	HSU802806	AL390149 Homo sapi
396	23	2.0	1799	9	AF035284	AF035284 Homo sapi	469	23	2.0	5142	9	AK000086	AK000086 Homo sapi
397	23	2.0	1810	9	AF218011	AF218011 Homo sapi	470	23	2.0	5541	9	HSU7599C	AF157814 Homo sapi
398	23	2.0	1828	8	CENCHRA1	X83887 C. elegans m	471	23	2.0	5797	9	HSU7599C	AF157814 Homo sapi
399	23	2.0	1832	8	BJY10848	Y10848 Brassica ju	472	23	2.0	7836	9	HSPB3D11	AL008640 Homo DNA
400	23	2.0	1853	9	AY007104	AY007104 Homo sapi	473	23	2.0	8170	9	ARI137242	AF137242 Sequence
401	23	2.0	1872	3	AF070920	AF070920 Caenorhab	474	23	2.0	9521	6	ARI137242	AF137242 Sequence
402	23	2.0	1874	6	AX008640	AX008640 Sequence	475	23	2.0	9951	6	AE001498	AE001498 Helicobac
403	23	2.0	1874	8	AF215854	AF215854 Zea mays	476	23	2.0	10094	1	AE001498	AE001498 Helicobac
404	23	2.0	1886	9	BC004526	BC004526 Homo sapi	477	23	2.0	11282	6	AC014906	AC014906 Drosophil
405	23	2.0	1893	9	AF070573	AF070573 Homo sapi	478	23	2.0	11282	6	AC014906	AC014906 Drosophil
406	23	2.0	1896	9	BC007846	BC007846 Homo sapi	479	23	2.0	11282	6	AC014906	AC014906 Drosophil
407	23	2.0	1914	9	HSU49396	U9396 Human Ionot	480	23	2.0	11282	6	AC014906	AC014906 Drosophil
408	23	2.0	1948	10	AF260582	AF260582 Rattus no	481	23	2.0	12029	3	AE001416	AE001416 Plasmodiu
409	23	2.0	1978	9	AF016709	AF016709 Homo sapi	482	23	2.0	13535	3	AE001416	AE001416 Plasmodiu
410	23	2.0	1986	9	HSU49395	U49395 Human Ionot	483	23	2.0	13535	3	AE001416	AE001416 Plasmodiu
411	23	2.0	2017	9	AB050415	AB050415 Macaca fa	484	23	2.0	13535	3	AE001416	AE001416 Plasmodiu
412	23	2.0	2051	10	AB041540	AB041540 Mus muscu	485	23	2.0	16556	6	AR043384	AR043384 Sequence
413	23	2.0	2062	10	AB041550	AB041550 Mus muscu	486	23	2.0	16556	6	AR043384	AR043384 Sequence
414	23	2.0	2064	9	HSU92544	U92544 Human hepat	487	23	2.0	16556	6	AR043384	AR043384 Sequence
415	23	2.0	2069	9	AF339775	AF339775 Homo sapi	488	23	2.0	18177	2	AC013876	AC013876 Drosophil
416	23	2.0	2077	9	BC000304	BC000304 Homo sapi	489	23	2.0	18705	3	CEY2686A	AL023830 Caenorhab
417	23	2.0	2079	9	AB047878	AB047878 Macaca fa	490	23	2.0	24643	8	SPAC6C3	U62292 Human elast
418	23	2.0	2092	9	HSU58089	U58089 Human Hs-cu	491	23	2.0	24643	8	SPAC6C3	U62292 Human elast
419	23	2.0	2108	9	BC010743	BC010743 Homo sapi	492	23	2.0	24643	8	SPAC6C3	U62292 Human elast
420	23	2.0	2133	6	A93395	A93395 Sequence 1	493	23	2.0	24643	8	SPAC6C3	U62292 Human elast
421	23	2.0	2185	10	BC005633	BC005633 Mus muscu	494	23	2.0	24643	8	SPAC6C3	U62292 Human elast
422	23	2.0	2203	9	AK025632	AK025632 Homo sapi	495	23	2.0	27500	3	CELF5AC4	AL355855 Human DNA
423	23	2.0	2209	9	BC002471	BC002471 Homo sapi	496	23	2.0	27500	3	CELF5AC4	AL355855 Human DNA
424	23	2.0	2219	9	AF181875	AF181875 Homo sapi	497	23	2.0	29442	9	AL355855	AL355855 Human DNA
425	23	2.0	2220	3	DFCAMP1	X52688 D. discoideu	498	23	2.0	29856	8	AC007311	AC007311 Arabidops
426	23	2.0	2241	3	AF063244	AF063244 Caenorhab	499	23	2.0	30824	9	AC016911	AC016911 Homo sapi
427	23	2.0	2241	3	AF063244	AF063244 Caenorhab	500	23	2.0	32256	2	AL513169	AL513169 Homo sapi
428	23	2.0	2255	3	AF201905	AF201905 Drosophil	501	23	2.0	32256	2	AL513169	AL513169 Homo sapi
429	23	2.0	2262	3	AF132194	AF132194 Cupienniu	502	23	2.0	33917	9	AC004410	AC004410 Homo sapi
430	23	2.0	2287	3	CSA307910	AJ307910 Cupienniu	503	23	2.0	34688	9	AC005759	AC005759 Homo sapi
431	23	2.0	2328	9	BC002791	BC002791 Homo sapi	504	23	2.0	35776	3	AF067946	AF067946 Caenorhab
432	23	2.0	2367	9	HSU801132	AL117598 Homo sapi	505	23	2.0	35776	3	AF067946	AF067946 Caenorhab
433	23	2.0	2373	6	I771100	I771100 Sequence 1	506	23	2.0	36302	3	CEXC482	AF025467 Caenorhab
434	23	2.0	2393	9	BC001957	BC001957 Homo sapi	507	23	2.0	37154	9	HS316G12	AL031709 Human DNA
435	23	2.0	2455	5	AF022890	AF022890 Gallus ga	508	23	2.0	37476	9	HS316G12	AL031709 Human DNA

509	23	2.0	41151	3	CEC48B4	229117 Caenorhabdi	c 582	23	2.0	71752	2	AC080173	AC080173 Homo sapi
c 510	23	2.0	41442	3	CBRG45N14	AC084650 Caenorhab	c 583	23	2.0	72383	2	AC027746	AC027746 Homo sapi
c 511	23	2.0	41617	2	AC004213	AC004213 Homo sapi	584	23	2.0	72383	2	AC027746	AC027746 Homo sapi
c 512	23	2.0	41921	2	AC068358	AC068358 Homo sapi	585	23	2.0	73029	2	AC018401	AC018401 Homo sapi
c 513	23	2.0	42559	9	AC005238	AC005238 Homo sapi	c 586	23	2.0	73029	2	HSBA329J7	AL118497 Human DNA
c 514	23	2.0	42831	9	AL512344	AL512344 Human DNA	587	23	2.0	73840	8	AB007644	AB007644 Arabidops
c 515	23	2.0	43297	9	AC005578	AC005578 Homo sapi	588	23	2.0	74012	9	AL136159	AL136159 Human DNA
c 516	23	2.0	43368	9	AC006162	AC006162 Homo sapi	589	23	2.0	74037	9	HS1071N3	AL031728 Human DNA
c 517	23	2.0	44653	9	HS380F5	AL031719 Human DNA	590	23	2.0	74154	2	AF274853	AF274853 Homo sapi
c 518	23	2.0	45437	2	AC002095	AC002095 Homo sapi	c 591	23	2.0	74174	2	AF003998	AF003998 Oryza sat
c 519	23	2.0	45829	2	AC092300	AC092300 Homo sapi	c 592	23	2.0	74516	2	AC025641	AC025641 Homo sapi
c 520	23	2.0	45928	2	CEIC13F7	281466 Caenorhabdi	c 593	23	2.0	75499	9	HSJ965G21	AL121772 Human DNA
c 521	23	2.0	47703	3	CEIC32D5	U23511 Caenorhabdi	c 594	23	2.0	75533	2	AC006412	AC006412 Homo sapi
c 522	23	2.0	47859	9	AP001469	AP001469 Homo sapi	595	23	2.0	75589	2	AC018536	AC018536 Homo sapi
c 523	23	2.0	48133	9	AL359700	AL359700 Human DNA	c 596	23	2.0	75793	9	HS321115	AL008632 Human DNA
c 524	23	2.0	48478	2	AC026687	AC026687 Homo sapi	c 597	23	2.0	76385	9	AC007033	AC007033 Homo sapi
c 525	23	2.0	49386	2	AC021257	AC021257 Homo sapi	c 598	23	2.0	76828	2	AC032029	AC032029 Homo sapi
c 526	23	2.0	51394	2	AC084133	AC084133 Homo sapi	c 599	23	2.0	76860	2	AC091631	AC091631 Homo sapi
c 527	23	2.0	51681	9	AP000261	AP000261 Homo sapi	c 600	23	2.0	76887	2	AC007775	AC007775 Homo sapi
c 528	23	2.0	51993	9	AC004951	AC004951 Homo sapi	c 601	23	2.0	77000	9	AP000795	AP000795 Homo sapi
c 529	23	2.0	52301	5	AB037997	AB037997 Danio rer	c 602	23	2.0	77083	9	AC008129	AC008129 Homo sapi
c 530	23	2.0	53823	2	AC091642	AC091642 Homo sapi	603	23	2.0	77835	2	PFMAL13P2_3	Continuation (4 of
c 531	23	2.0	54450	2	AC080179	AC080179 Homo sapi	604	23	2.0	77923	8	AC064840	AC064840 Arabidops
c 532	23	2.0	54594	9	AC073272	AC073272 Homo sapi	605	23	2.0	78089	3	AC024876	AC024876 Caenorhab
c 533	23	2.0	54649	9	AL135935	AL135935 Human DNA	c 606	23	2.0	78102	2	AC011408	AC011408 Homo sapi
c 534	23	2.0	56632	9	HS511E16	AL023694 Human DNA	c 607	23	2.0	78378	8	AC007260	AC007260 Arabidops
c 535	23	2.0	56725	9	AL451080	AL451080 Human DNA	608	23	2.0	79970	2	AC011428	AC011428 Homo sapi
c 536	23	2.0	57000	9	AB038162	AB038162 Homo sapi	609	23	2.0	80048	9	AC010143	AC010143 Homo sapi
c 537	23	2.0	57449	9	AL390768	AL390768 Human DNA	c 610	23	2.0	80292	9	HSJ879N19	AL109855 Human DNA
c 538	23	2.0	58628	9	AC027719	AC027719 Homo sapi	c 611	23	2.0	80343	9	HS474112	AL022333 Human DNA
c 539	23	2.0	59036	2	AC015505	AC015505 Homo sapi	c 612	23	2.0	80518	2	PFMAL13PA	AL109815 Plasmodi
c 540	23	2.0	59130	9	AL135904	AL135904 Human DNA	c 613	23	2.0	80561	8	AC073555	AC073555 Arabidops
c 541	23	2.0	59309	2	AC090996	AC090996 Homo sapi	c 614	23	2.0	80796	9	AC073136	AC073136 Homo sapi
c 542	23	2.0	60121	2	AC036198	AC036198 Homo sapi	c 615	23	2.0	80929	2	AC023159	AC023159 Homo sapi
c 543	23	2.0	60631	9	HS376823	AL031078 Human DNA	c 616	23	2.0	81223	8	T26D3	AF262043 Arabidops
c 544	23	2.0	60886	9	AL591969	AL591969 Human DNA	c 617	23	2.0	81365	8	AB025633	AB025633 Arabidops
c 545	23	2.0	61274	9	AL391815	AL391815 Human DNA	c 618	23	2.0	81566	9	AL353630	AL353630 Human DNA
c 546	23	2.0	61407	2	AC012414	AC012414 Homo sapi	c 619	23	2.0	81704	8	AC084807	AC084807 Arabidops
c 547	23	2.0	61550	2	AC069038	AC069038 Homo sapi	c 620	23	2.0	81786	9	AC003002	AC003002 Human DNA
c 548	23	2.0	62035	9	AC078937	AC078937 Homo sapi	c 621	23	2.0	82650	2	AF186999	AF186999 Homo sapi
c 549	23	2.0	62107	9	AL160257	AL160257 Human DNA	c 622	23	2.0	82812	9	HSJ764O22	AL096799 Human DNA
c 550	23	2.0	62416	2	AC073451	AC073451 Homo sapi	c 623	23	2.0	83039	9	AL137074	AL137074 Human DNA
c 551	23	2.0	62449	2	AC061985	AC061985 Homo sapi	c 624	23	2.0	83673	9	HSDA79C13	AL117325 Human DNA
c 552	23	2.0	62449	2	AC061985	AC061985 Homo sapi	c 625	23	2.0	83761	2	AC023061	AC023061 Homo sapi
c 553	23	2.0	62536	9	AC005692	AC005692 Homo sapi	c 626	23	2.0	84388	9	AL589984	AL589984 Human DNA
c 554	23	2.0	63334	2	AC032023	AC032023 Homo sapi	c 627	23	2.0	84847	2	AC074058	AC074058 Homo sapi
c 555	23	2.0	63638	2	AC020175	AC020175 Drosophila	c 628	23	2.0	85538	9	HS751D22	AL049565 Human DNA
c 556	23	2.0	63682	2	AL135782	AL135782 Homo sapi	c 629	23	2.0	86894	2	AL390319	AL390319 Homo sapi
c 557	23	2.0	64032	8	AC018722	AC018722 Arabidops	c 630	23	2.0	87258	9	AF091512	AF091512 Homo sapi
c 558	23	2.0	64151	9	AL139399	AL139399 Human DNA	c 631	23	2.0	87646	9	HS1048E9	299714 Human DNA s
c 559	23	2.0	64256	9	AC016758	AC016758 Homo sapi	c 632	23	2.0	87869	9	HS286B10	282244 Human DNA s
c 560	23	2.0	64579	2	AC068348	AC068348 Homo sapi	c 633	23	2.0	87947	8	AC006201	AC006201 Arabidops
c 561	23	2.0	65016	2	AC090620	AC090620 Homo sapi	c 634	23	2.0	88018	9	AC010418	AC010418 Homo sapi
c 562	23	2.0	65201	9	HS754E20A	AL096761 Human DNA	c 635	23	2.0	88473	9	AF191071	AF191071 Homo sapi
c 563	23	2.0	65417	2	AC027202	AC027202 Homo sapi	c 636	23	2.0	88672	2	AC032607	AC032607 Homo sapi
c 564	23	2.0	65599	2	AC090782	AC090782 Homo sapi	c 637	23	2.0	89372	2	AC090602	AC090602 Homo sapi
c 565	23	2.0	65760	2	AC040965	AC040965 Homo sapi	c 638	23	2.0	89820	9	AC007868	AC007868 Genomic S
c 566	23	2.0	67033	2	AC027371	AC027371 Homo sapi	c 639	23	2.0	89939	2	AC022667	AC022667 Homo sapi
c 567	23	2.0	67179	2	AC084787	AC084787 Homo sapi	c 640	23	2.0	90248	8	AC026480	AC026480 Arabidops
c 568	23	2.0	67209	2	AC090932	AC090932 Homo sapi	c 641	23	2.0	91334	2	AC024691	AC024691 Homo sapi
c 569	23	2.0	67550	2	AC016452	AC016452 Homo sapi	c 642	23	2.0	92611	9	AC006398	AC006398 Homo sapi
c 570	23	2.0	67711	2	AC090353	AC090353 Homo sapi	c 643	23	2.0	92644	2	AF186995	AF186995 Homo sapi
c 571	23	2.0	68531	2	AC055868	AC055868 Homo sapi	c 644	23	2.0	93187	2	AC021902	AC021902 Homo sapi
c 572	23	2.0	68581	2	AC027375	AC027375 Homo sapi	c 645	23	2.0	93764	2	AC074072	AC074072 Homo sapi
c 573	23	2.0	69334	2	AC004912	AC004912 Homo sapi	c 646	23	2.0	93764	2	AC074072	AC074072 Homo sapi
c 574	23	2.0	69660	9	HS407F17	283845 Human DNA s	c 647	23	2.0	94060	2	AF216673	AF216673 Homo sapi
c 575	23	2.0	69740	2	AC087748	AC087748 Homo sapi	c 648	23	2.0	94319	9	HS341110	297352 Human DNA s
c 576	23	2.0	69775	9	AC006347	AC006347 Homo sapi	c 649	23	2.0	94418	2	AC025058	AC025058 Homo sapi
c 577	23	2.0	70104	2	AC090812	AC090812 Homo sapi	c 650	23	2.0	94673	2	AC009018	AC009018 Homo sapi
c 578	23	2.0	70990	2	AC087854	AC087854 Homo sapi	c 651	23	2.0	95073	9	AC007272	AC007272 Homo sapi
c 579	23	2.0	71179	9	AL136110	AL136110 Human DNA	c 652	23	2.0	95546	8	AC022816	AC022816 Homo sapi
c 580	23	2.0	71509	9	AL589880	AL589880 Human DNA	c 653	23	2.0	95769	8	AC013430	AC013430 Genomic s
c 581	23	2.0	71509	9	AL589880	AL589880 Human DNA	c 654	23	2.0	96948	2	AC084728	AC084728 Homo sapi

655	23	2.0	97385	9	HSJ447F3	AL050348	Human DNA	728	23	2.0	113762	9	AC005294	Homo sapi
656	23	2.0	97845	9	AL355337	AL355337	Human DNA	c 729	23	2.0	114003	9	AC008547	Homo sapi
657	23	2.0	98339	9	AL390295	AL390295	Human DNA	730	23	2.0	114149	9	AC022083	Homo sapi
658	23	2.0	98362	9	AL390295	AL390295	Human DNA	c 731	23	2.0	114194	2	AC093200	Homo sapi
659	23	2.0	98393	2	AL356472	AL356472	Human DNA	732	23	2.0	114258	2	AP000671	Homo sapi
660	23	2.0	98393	2	AL356472	AL356472	Human DNA	c 733	23	2.0	114351	2	AC006875	Homo sapi
661	23	2.0	98776	9	HSJ90108	AL078461	Human DNA	c 734	23	2.0	114364	9	AC011666	Human Chr
662	23	2.0	99887	2	AC026481	AC026481	Human sapi	c 735	23	2.0	114526	9	HSJ1043F6	Human DNA
663	23	2.0	100000	9	AB020877	AB020877	Human sapi	736	23	2.0	114842	9	AC002996	Homo sapi
664	23	2.0	100000	9	AP000035	AP000035	Human sapi	737	23	2.0	115218	9	HS159A1	Human DNA
665	23	2.0	100000	9	AP000075	AP000075	Human sapi	738	23	2.0	115304	9	AL138775	Human DNA
666	23	2.0	100000	9	AP000100	AP000100	Human sapi	739	23	2.0	115327	2	AL138775	Human sapi
667	23	2.0	100000	9	AP000127	AP000127	Human sapi	c 740	23	2.0	117502	2	AP000442	Homo sapi
668	23	2.0	100000	9	AP000176	AP000176	Human sapi	741	23	2.0	117602	2	AC007055	Homo sapi
669	23	2.0	100000	9	AP000205	AP000205	Human sapi	c 742	23	2.0	118195	9	AC007899	Homo sapi
670	23	2.0	100288	2	AP001945	AP001945	Human sapi	743	23	2.0	118357	9	HS1142C11	Human DNA
671	23	2.0	100296	9	AL590308	AL590308	Human DNA	744	23	2.0	118524	9	HS1142C11	Human DNA
672	23	2.0	100925	9	AC012637	AC012637	Human sapi	745	23	2.0	118595	9	AC002379	Human BAC
673	23	2.0	100983	2	AP003840	AP003840	Oryza sat	746	23	2.0	119349	9	AC020934	Homo sapi
674	23	2.0	101041	2	AP002079	AP002079	Human sapi	747	23	2.0	119790	9	HSJ989D7	Human DNA
675	23	2.0	101216	2	AC060227	AC060227	Human sapi	748	23	2.0	120112	9	AC012355	Homo sapi
676	23	2.0	101245	2	AC079338	AC079338	Human sapi	749	23	2.0	120829	2	AC009829	Homo sapi
677	23	2.0	101629	2	AC010023	AC010023	Drosophila	c 750	23	2.0	121086	5	AL590146	Human DNA
678	23	2.0	101685	9	HSJ39622	AL050341	Human DNA	751	23	2.0	121606	9	AL160401	Human DNA
679	23	2.0	101830	9	AL359454	AL359454	Human DNA	752	23	2.0	122103	9	HS291J10	Human DNA
680	23	2.0	102135	8	AC069144	AC069144	Arabidops	c 753	23	2.0	122638	9	AB001523	Homo sapi
681	23	2.0	102703	9	AC004910	AC004910	Human sapi	c 754	23	2.0	122732	2	HS436C18	Homo sapi
682	23	2.0	103115	9	AC026440	AC026440	Human sapi	c 755	23	2.0	123339	2	AF179296	Homo sapi
683	23	2.0	103153	9	AC010340	AC010340	Human sapi	c 756	23	2.0	123695	9	HSJ581I13	Human DNA
684	23	2.0	103649	2	AL445219	AL445219	Human sapi	c 757	23	2.0	124230	2	AL591742	Homo sapi
685	23	2.0	103740	9	HSJ102H19	AL096817	Human DNA	c 758	23	2.0	124439	2	AL603717	Homo sapi
686	23	2.0	103779	2	AC073239	AC073239	Human sapi	c 759	23	2.0	124441	2	AC027098	Homo sapi
687	23	2.0	103788	9	AC008643	AC008643	Human sapi	c 760	23	2.0	124667	2	AC015568	Homo sapi
688	23	2.0	103826	9	AL139339	AL139339	Human DNA	c 761	23	2.0	124845	2	AL353172	Homo sapi
689	23	2.0	104086	3	AE003567	AE003567	Drosophila	c 762	23	2.0	124876	9	AC004167	Homo sapi
690	23	2.0	104848	2	AC004588	AC004588	Homo sapi	c 763	23	2.0	124927	2	AC010475	Homo sapi
691	23	2.0	104913	9	AC004242	AC004242	Human sapi	c 764	23	2.0	125000	2	AB017602	Homo sapi
692	23	2.0	105080	9	AC026439	AC026439	Human sapi	c 765	23	2.0	125204	2	AL163540	Homo sapi
693	23	2.0	106168	9	AC011450	AC011450	Human sapi	c 766	23	2.0	125295	2	AF186998	Homo sapi
694	23	2.0	106486	2	AC011805	AC011805	Human sapi	c 767	23	2.0	125373	9	AL353707	Human DNA
695	23	2.0	106534	9	AL355609	AL355609	Human DNA	c 768	23	2.0	125376	9	AP001627	Homo sapi
696	23	2.0	106806	2	AF165177	AF165177	Human sapi	c 769	23	2.0	125439	9	AC010485	Homo sapi
697	23	2.0	107159	9	HS422F24	AL031010	Human DNA	c 770	23	2.0	125653	9	AL133517	Human DNA
698	23	2.0	107264	9	AP002078	AP002078	Human sapi	c 771	23	2.0	126266	2	AC008885	Homo sapi
699	23	2.0	107387	9	HS07K17	AL024473	Human DNA	c 772	23	2.0	126367	9	AL136109	Human DNA
700	23	2.0	107418	9	HS551E13	AL022163	Human DNA	c 773	23	2.0	126392	2	AC018785	Homo sapi
701	23	2.0	107429	9	HSJ21420	AL121969	Human DNA	c 774	23	2.0	126392	2	AC018785	Homo sapi
702	23	2.0	108124	2	AL157948	AL157948	Human sapi	c 775	23	2.0	126464	9	HS225E12	Human DNA
703	23	2.0	108765	2	AF216674	AF216674	Human sapi	c 776	23	2.0	126883	2	AC008832	Homo sapi
704	23	2.0	108803	9	HS550H1	AL035420	Human DNA	c 777	23	2.0	127661	2	AP001261	Homo sapi
705	23	2.0	109395	2	AC013742	AC013742	Human sapi	c 778	23	2.0	127867	9	HS694B14	Human DNA
706	23	2.0	109723	2	AP000633	AP000633	Human sapi	c 779	23	2.0	128289	9	AC007972	Homo sapi
707	23	2.0	110000	2	AC003656_5	Continuation (6 of	780	23	2.0	128328	9	AC005839	Homo sapi	
708	23	2.0	110000	2	AC008749_2	Continuation (3 of	781	23	2.0	128386	9	AL356782	Human DNA	
709	23	2.0	110000	2	AL57379_2	Continuation (3 of	782	23	2.0	128501	9	AC004675	Homo sapi	
710	23	2.0	110000	2	AL359978_1	Continuation (2 of	c 783	23	2.0	128524	2	AC012253	Homo sapi	
711	23	2.0	110000	2	CEV111B2_3	Continuation (4 of	c 784	23	2.0	128554	9	AL162500	Human DNA	
712	23	2.0	110000	2	AC015850_2	Continuation (3 of	c 785	23	2.0	128563	2	AC078792	Homo sapi	
713	23	2.0	110000	33	AP002753_2	Continuation (3 of	786	23	2.0	128590	2	AC009557	Homo sapi	
714	23	2.0	110034	2	AF188024	AF188024	Homo sapi	787	23	2.0	128680	2	AC023374	Homo sapi
715	23	2.0	110096	9	CHI9HHR23	AD000092	Homo sapi	788	23	2.0	128757	9	AL359837	Human DNA
716	23	2.0	110159	2	AC068178	AC068178	Human sapi	c 789	23	2.0	128822	2	AP001260	Homo sapi
717	23	2.0	110794	9	AL133268	AL133268	Human DNA	c 790	23	2.0	128960	2	HSJ919F19	Human DNA
718	23	2.0	111051	9	AL353806	AL353806	Human DNA	791	23	2.0	129402	2	AP002825	Homo sapi
719	23	2.0	111073	9	AC006375	AC006375	Homo sapi	792	23	2.0	129625	9	AC009301	Homo sapi
720	23	2.0	111107	9	AC005924	AC005924	Homo sapi	c 793	23	2.0	130077	9	AL353643	Human DNA
721	23	2.0	111942	9	AP004016	AP004016	Homo sapi	c 794	23	2.0	130142	2	AC017890	Drosophila
722	23	2.0	112270	9	AP002002	AP002002	Homo sapi	c 795	23	2.0	130617	2	AC026793	Homo sapi
723	23	2.0	112356	9	AL138812	AL138812	Human DNA	c 796	23	2.0	130831	2	AC027568	Homo sapi
724	23	2.0	112539	9	AL356455	AL356455	Homo sapi	c 797	23	2.0	130855	9	AC004089	Homo sapi
725	23	2.0	112808	2	AC068024	AC068024	Homo sapi	798	23	2.0	131074	2	AC008807	Homo sapi
726	23	2.0	112986	2	AF215841	AF215841	Homo sapi	c 799	23	2.0	131156	2	AC015934	Homo sapi
727	23	2.0	113189	9	AC007883	AC007883	Homo sapi	c 800	23	2.0	131159	2	AP000743	Homo sapi

801	23	2.0 131161	2	AC068938	Homo sapi
802	23	2.0 131535	9	AC005875	ctib-188-
c 803	23	2.0 131611	9	AC005099	Homo sapi
804	23	2.0 131612	9	AL353771	Human DNA
805	23	2.0 131684	9	AL137849	Human DNA
806	23	2.0 131716	2	AC025833	Homo sapi
807	23	2.0 131975	9	AC008940	Homo sapi
808	23	2.0 132124	2	AC004737	Homo sapi
c 809	23	2.0 132128	2	AC008851	Homo sapi
c 810	23	2.0 132590	2	AL355483	Homo sapi
c 811	23	2.0 132916	9	AC018765	Homo sapi
c 812	23	2.0 133370	2	AF172273	Homo sapi
813	23	2.0 134466	2	AC068417	Homo sapi
c 814	23	2.0 134534	2	AL512352	Homo sapi
815	23	2.0 134540	2	AC090898	Homo sapi
816	23	2.0 134579	2	AC078999	Homo sapi
c 817	23	2.0 134784	2	AC061992	Homo sapi
818	23	2.0 134845	9	HS863K19	Human DNA
c 819	23	2.0 134946	2	AC069568	Homo sapi
c 820	23	2.0 135240	9	AL136362	Human DNA
c 821	23	2.0 135255	2	AC013804	Homo sapi
c 822	23	2.0 135354	9	AC010627	Homo sapi
c 823	23	2.0 135521	9	AC005858	Homo sapi
c 824	23	2.0 136198	2	AL392004	Homo sapi
825	23	2.0 136492	9	AC011143	Homo sapi
826	23	2.0 136503	2	AC068939	Homo sapi
c 827	23	2.0 136590	2	AF161326	Homo sapi
c 828	23	2.0 136712	2	AC009630	Homo sapi
c 829	23	2.0 136747	2	AC074389	Homo sapi
c 830	23	2.0 136911	2	AL135843	Homo sapi
c 831	23	2.0 136968	9	AL390788	Human DNA
c 832	23	2.0 137074	9	AF130248	Homo sapi
c 833	23	2.0 137496	9	AC005288	Homo sapi
c 834	23	2.0 137496	9	AC005288	Homo sapi
c 835	23	2.0 137622	2	AC008694	Homo sapi
c 836	23	2.0 137701	9	AC079088	Homo sapi
c 837	23	2.0 137737	9	AC010378	Homo sapi
c 838	23	2.0 138129	2	AC011036	Homo sapi
c 839	23	2.0 138177	2	AC021931	Homo sapi
c 840	23	2.0 138490	10	MMU249895	Mus muscu
c 841	23	2.0 138872	2	AC027560	Homo sapi
c 842	23	2.0 138876	2	AL590067	Homo sapi
c 843	23	2.0 138993	2	AC087653	Homo sapi
844	23	2.0 139266	2	AC068747	Homo sapi
c 845	23	2.0 139290	2	AC068096	Homo sapi
c 846	23	2.0 139361	2	AL357056	Homo sapi
c 847	23	2.0 139523	2	AC040932	Homo sapi
c 848	23	2.0 139633	9	AC022201	Homo sapi
c 849	23	2.0 140161	2	AL390725	Homo sapi
c 850	23	2.0 140179	2	AC084688	Homo sapi
c 851	23	2.0 140256	9	AC004972	Homo sapi
c 852	23	2.0 140271	2	AC090888	Homo sapi
c 853	23	2.0 140597	9	AC074270	Homo sapi
c 854	23	2.0 140628	2	AC016468	Homo sapi
c 855	23	2.0 140965	9	AC005587	Homo sapi
c 856	23	2.0 140966	9	AC023058	Homo sapi
c 857	23	2.0 141056	9	AL354836	Human DNA
c 858	23	2.0 141347	9	AC083820	Rattus no
c 859	23	2.0 141371	9	AC010319	Homo sapi
c 860	23	2.0 141372	2	AC011779	Homo sapi
c 861	23	2.0 141378	2	AC069281	Homo sapi
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c 863	23	2.0 141870	2	AC092986	Homo sapi
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c 865	23	2.0 142185	2	AC022656	Homo sapi
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c 868	23	2.0 142396	2	AC093211	Homo sapi
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c 871	23	2.0 143259	2	AC084334	Homo sapi
c 872	23	2.0 143321	2	AC021419	Homo sapi
c 873	23	2.0 143405	2	AC062023	Homo sapi

c 874	23	2.0 143463	9	AL139243	Human DNA
c 875	23	2.0 143498	2	AC019348	Homo sapi
c 876	23	2.0 143553	9	AC010234	Homo sapi
c 877	23	2.0 143561	2	AC046191	Homo sapi
c 878	23	2.0 143689	2	AC018374	Homo sapi
c 879	23	2.0 143812	2	AC021847	Homo sapi
c 880	23	2.0 144162	2	AC008434	Homo sapi
c 881	23	2.0 144248	2	AL133291	Homo sapi
c 882	23	2.0 144348	2	AC016423	Homo sapi
c 883	23	2.0 144437	2	AC019273	Homo sapi
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c 885	23	2.0 144794	2	AC087632	Homo sapi
c 886	23	2.0 145013	2	AC093301	Homo sapi
c 887	23	2.0 145063	2	AC027069	Homo sapi
c 888	23	2.0 145272	2	AC016938	Homo sapi
c 889	23	2.0 145382	2	AC073223	Homo sapi
c 890	23	2.0 145392	2	AC009923	Homo sapi
c 891	23	2.0 145414	9	HS392M18	Human DNA
c 892	23	2.0 145520	2	AC016036	Homo sapi
c 893	23	2.0 145650	2	AC068777	Homo sapi
c 894	23	2.0 145762	9	AP001626	Homo sapi
c 895	23	2.0 145899	2	AC016611	Homo sapi
c 896	23	2.0 145917	2	AL139154	Homo sapi
c 897	23	2.0 146017	2	AC027473	Homo sapi
c 898	23	2.0 146190	2	AC073826	Mus muscu
c 899	23	2.0 146197	2	AC009722	Homo sapi
c 900	23	2.0 146233	9	AC016594	Homo sapi
c 901	23	2.0 146255	2	AC084170	Homo sapi
c 902	23	2.0 146523	2	AL512643	Homo sapi
c 903	23	2.0 146877	2	AC026487	Homo sapi
c 904	23	2.0 147168	2	AC080067	Homo sapi
c 905	23	2.0 147233	2	AC087486	Homo sapi
c 906	23	2.0 147250	2	AC011778	Homo sapi
c 907	23	2.0 147260	2	AC016340	Homo sapi
c 908	23	2.0 147724	9	HS395P12	Human DNA
c 909	23	2.0 147771	2	AC021860	Homo sapi
c 910	23	2.0 147806	2	AC092701	Homo sapi
c 911	23	2.0 147913	2	AC026971	Homo sapi
c 912	23	2.0 147924	2	AC036186	Homo sapi
c 913	23	2.0 147999	2	AL161635	Homo sapi
c 914	23	2.0 148122	9	AC084816	Homo sapi
c 915	23	2.0 148308	2	AC084703	Homo sapi
c 916	23	2.0 148334	2	AC087106	Homo sapi
c 917	23	2.0 148464	2	AL139245	Homo sapi
c 918	23	2.0 148496	2	AC079332	Homo sapi
c 919	23	2.0 148508	2	AC027795	Homo sapi
c 920	23	2.0 148565	2	AC023793	Homo sapi
c 921	23	2.0 148774	2	AL591423	Homo sapi
c 922	23	2.0 148819	9	AC006996	Homo sapi
c 923	23	2.0 149181	2	AL590487	Homo sapi
c 924	23	2.0 149384	9	AC006318	Homo sapi
c 925	23	2.0 149545	2	AC021984	Homo sapi
c 926	23	2.0 149898	9	AP000244	Homo sapi
c 927	23	2.0 149948	2	AC068852	Homo sapi
c 928	23	2.0 150151	9	AL356115	Human DNA
c 929	23	2.0 150236	9	HS101G11	Human DNA
c 930	23	2.0 150275	2	AC080068	Homo sapi
c 931	23	2.0 150332	9	AC004921	Homo sapi
c 932	23	2.0 150399	2	AC013385	Homo sapi
c 933	23	2.0 150436	2	AC024119	Homo sapi
c 934	23	2.0 150513	2	AC046158	Homo sapi
c 935	23	2.0 150647	2	AF311104	Homo sapi
c 936	23	2.0 150725	2	AC019044	Homo sapi
c 937	23	2.0 150751	2	AC020583	Homo sapi
c 938	23	2.0 150788	2	AC011832	Homo sapi
c 939	23	2.0 150938	2	AC025293	Homo sapi
c 940	23	2.0 151024	2	AC016855	Homo sapi
c 941	23	2.0 151068	9	AL133405	Human DNA
c 942	23	2.0 151097	2	AC083846	Homo sapi
c 943	23	2.0 151162	2	AC009364	Homo sapi
c 944	23	2.0 151358	2	AL590437	Human Chr
c 945	23	2.0 151415	2	AL596257	Homo sapi
c 946	23	2.0 151553	9	AL139342	Human DNA

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947 2.0 151611 2 AP001131
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949 2.0 151846 2 AC024366 Homo sapi
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952 2.0 152103 2 AC012130
953 2.0 152145 2 AC069570 Homo sapi
954 2.0 152395 2 AC013488 Homo sapi
955 2.0 152464 2 AC027421 Homo sapi
956 2.0 152488 2 AC063943 Homo sapi
957 2.0 152528 2 AC016063 Homo sapi
958 2.0 152537 9 AC055731 Homo sapi
959 2.0 152622 2 AC002253 Homo sapi
960 2.0 152623 9 AC011595 Homo sapi
961 2.0 152741 2 AC021606 Homo sapi
962 2.0 152816 2 AC079739 Homo sapi
963 2.0 153025 2 AC087533 Homo sapi
964 2.0 153046 9 AL590009 Human DNA
965 2.0 153137 9 AC016995 Homo sapi
966 2.0 153267 2 AC011212 Homo sapi
967 2.0 153289 2 AC013533 Homo sapi
968 2.0 153386 2 AC011933 Homo sapi
969 2.0 153566 2 AL161895 Homo sapi
970 2.0 153605 2 AC019360 Homo sapi
971 2.0 153652 2 AC092767 Homo sapi
972 2.0 153688 9 AC073225 Homo sapi
973 2.0 153693 9 AC010373 Homo sapi
974 2.0 153767 2 AC079972 Homo sapi
975 2.0 153855 2 AC092524 Homo sapi
976 2.0 153920 2 AC011723 Homo sapi
977 2.0 154257 2 AC025803 Homo sapi
978 2.0 154286 9 AC016698 Homo sapi
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980 2.0 154608 2 AC073620 Homo sapi
981 2.0 154685 9 AC007214 Pan trogl
982 2.0 154746 2 AL390733 Homo sapi
983 2.0 154747 2 AC068826 Homo sapi
984 2.0 154846 2 AP001374 Homo sapi
985 2.0 154904 9 AL162272 Human DNA
986 2.0 155030 9 AL357992 Human DNA
987 2.0 155278 9 HSD3655C4
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989 2.0 155559 2 AL133336 Homo sapi
990 2.0 155577 2 AC011565 Homo sapi
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992 2.0 155663 2 AC069238 Homo sapi
993 2.0 155691 2 AC023214 Homo sapi
994 2.0 155740 2 AC025003 Homo sapi
995 2.0 155744 2 AL157784 Homo sapi
996 2.0 155749 2 AC021785 Homo sapi
997 2.0 155779 2 AC068260 Homo sapi
998 2.0 155789 2 AC015726 Homo sapi
999 2.0 155869 2 AC023420 Homo sapi
1000 2.0 156000 2 AC060815 Homo sapi

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ALIGNMENTS

```

RESULT 1
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LOCUS AC064803 214005 bp DNA HTG 09-MAY-2001
DEFINITION Mus musculus chromosome 11 clone RP23-16G14 map 11, WORKING DRAFT
SEQUENCE 15 unordered pieces.
AC064803.3 GI:12061538
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 214005)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.

```

TITLE

JOURNAL
REFERENCE
AUTHORS

Mus musculus chromosome 11, clone RP23-16G14
Unpublished
2 (bases 1 to 214005)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavskiy,L., Boukhalter,B., Brown,A., Burkett,G.,
Campoliano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collamore,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRoque,K., Lamazares,R., Landers,T., Lehotzky,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
McElrath,J., Menes,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talanas,J.,
Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.

TITLE
JOURNAL
COMMENT

Direct Submission
Submitted (22-APR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jan 10, 2001 this sequence version replaced gi:10122086.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence.submissions@genome.wi.mit.edu

----- Project Information

Center project name: 16_G14

----- Summary Statistics

Sequencing vector: M13; M7815; 55% of reads

Sequencing vector: Plasmid; n/a; 45% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 208302 bases at least Q40

Consensus quality: 210581 bases at least Q30

Consensus quality: 211578 bases at least Q20

Insert size: 197000; agarose-fp

Insert size: 212605; sum-of-contigs

Quality coverage: 8.3 in Q20 bases; agarose-fp

Quality coverage: 7.7 in Q20 ba.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 21460: contig of 21460 bp in length
* 21461 21560: gap of 100 bp
* 21561 24845: contig of 3285 bp in length
* 24846 24945: gap of 100 bp
* 24946 28115: contig of 3170 bp in length
* 28116 28215: gap of 100 bp
* 28216 36178: contig of 7963 bp in length
* 36179 36278: gap of 100 bp
* 36279 43409: contig of 7131 bp in length
* 43410 43509: gap of 100 bp
* 43510 52058: contig of 8549 bp in length
* 52059 52158: gap of 100 bp
* 52159 91851: contig of 39693 bp in length
* 91852 91951: gap of 100 bp

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* 91952 104472: contig of 12521 bp in length
* 10473 104572: gap of 100 bp
* 104573 117147: contig of 12575 bp in length
* 117148 117247: gap of 100 bp
* 117248 129469: contig of 12222 bp in length
* 129470 129569: gap of 100 bp
* 129570 143560: contig of 13991 bp in length
* 143561 143660: gap of 100 bp
* 143661 159711: contig of 16051 bp in length
* 159712 159811: gap of 100 bp
* 159812 178155: contig of 18344 bp in length
* 178156 178255: gap of 100 bp
* 178256 200956: contig of 22701 bp in length
* 200957 201056: gap of 100 bp
* 201057 214005: contig of 12949 bp in length.

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FEATURES

source

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24946. 28115
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36279. 43409
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BASE COUNT 52714 a 53509 c 53045 g 53279 t 1458 others
ORIGIN

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Query Match 2.6%; Score 30; DB 2: Length 214005;
Best Local Similarity 100.08; Pred. No. 0.00021;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1144 tgagattatttcaaaaaaaaaaaaaaaaaa 1173
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Db 91303 TGAGATTATTTCAAAAAAAAAAAAAAAAA 91274

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RESULT 2
AC041023/C. AC041023 185996 bp DNA HTG 22-MAY-2000
LOCUS

```

DEFINITION

Homo sapiens clone RP11-356G3, WORKING DRAFT SEQUENCE, 20 unordered pieces.

AC041023

VERSION AC041023.2 GI:8016758

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.

SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 185996)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens, clone RP11-356G3

Unpublished

2 (bases 1 to 185996)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavsky, L., Boukhgaltier, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeAtellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrum, J., Meneus, L., Mihova, T., Miranda, C., Mienna, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission

TITLE

JOURNAL

COMMENT

Submitted (11-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 22, 2000 this sequence version replaced gi:7534225.
All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L9601

Center clone name: 356_G_3

----- Summary Statistics

Sequencing vector: M13; M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 175155 bases at least Q40

Consensus quality: 180623 bases at least Q30

Consensus quality: 182712 bases at least Q20

Insert size: 188000; agarose-fp

Insert size: 184096; sum-of-contigs

Quality coverage: 4.5 in Q20 bases; agarose-fp

Quality coverage: 4.6 in Q20 bases; sum-of-contigs

----- NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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* 1 2941: contig of 2941 bp in length
* 2942 3041: gap of 100 bp
* 3042 5193: contig of 2152 bp in length

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Best Local Similarity 100.0%; Pred. No. 0.00071;				
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1145 gagattttttcaaaaaaaaaaaaaaaaaa 1173			
Db	28852 GAGATTATTTCAAAAAAAAAAAAAAAAAA 28824			
RESULT	3			
LES133600	LES133600 602 bp mRNA PLN 04-MAY-1999			
LOCUS	Lycopersicon esculentum mRNA for extensin-like protein.			
DEFINITION	AJ133600			
ACCESSION	AJ133600.1 GI:4753794			
VERSION	extensin-like protein.			
KEYWORDS	tomato.			
SOURCE	Lycopersicon esculentum			
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.			
REFERENCE	1 (bases 1 to 602)			
AUTHORS	van den Heuvel,K.J.P.T., van Lipzig,R.H.A., Barendse,G.W.M. and Willems,G.J.			
TITLE	Characterization of two flower specific cDNAs which expression is regulated by gibberellin in tomato (Lycopersicon esculentum)			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 602)			
AUTHORS	van den Heuvel,K.J.P.T.			
TITLE	Direct Submission			
JOURNAL	Submitted (04-MAR-1999); van den Heuvel K.J.P.T., Experimental Botany, University of Nijmegen, Toernooiveld 1, 6525 ED Nijmegen, NETHERLANDS			
FEATURES	Location/Qualifiers			
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	/tissue_lib="gib-1 anther library"			
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	/clone="TGAS105"			
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CDS	11..424			
	/codon_start=1			
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	/protein_id="CAB42005.1"			
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EOLKOIRKQKLIHLFQSGVLKTSYHWDKGYFFISYNNKVSQTVVDSEFTTKRKQK
YIDKIKDLKDKSEKCATPOLNFRFPNPNYSVSAKNSGNQK"

Qy 1148 attatttcaaaaaa 1173
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Db 577 ATTATTTCAAAAAA 1044 t

Query Match      2.2%; Score 26; DB 3; Length 2518;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1148 attatttcaaaaaa 1173
|||||
Db 1555 ATTATTTCAAAAAA 1580

RESULT 5
AF145620
LOCUS
DEFINITION
Drosophila melanogaster clone GH03922 BCDNA.GH03922)
ACCESSION
AF145620.1 GI:5052529
VERSION
FLI.CDNA.
KEYWORDS
fruit fly.
SOURCE
Drosophila melanogaster
ORGANISM
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 2580)
Rubin,G.M., Wan,K.H., Harvey,D., Lewis,S.E., Brokstein,P.,
Tsang,G., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
Butenhoff,C., Champe,M., Chavez,C., Chew,M., Doyle,C.M.,
Farfan,D.E., Frise,E., Galle,R., George,R.A., Harris,N.L.,
Hoskins,R.A., Evans-Holm,M., Houston,K.A., Hummasti,S.R., Kim,E.,
Li,P., Moshrefi,M., Pacleb,J.M., Park,S., Sequeira,A., Sethi,H.,
Snir,E., Swirskas,R.R., Weinburg,T. and Celniker,S.E.
Full length Drosophila melanogaster cDNA sequence
Unpublished
JOURNAL
REFERENCE
2 (bases 1 to 2580)
Rubin,G.M., Wan,K.H., Harvey,D., Lewis,S.E., Brokstein,P.,
Tsang,G., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
Butenhoff,C., Champe,M., Chavez,C., Chew,M., Doyle,C.M.,
Farfan,D.E., Frise,E., Galle,R., George,R.A., Harris,N.L.,
Hoskins,R.A., Evans-Holm,M., Houston,K.A., Hummasti,S.R., Kim,E.,
Li,P., Moshrefi,M., Pacleb,J.M., Park,S., Sequeira,A., Sethi,H.,
Snir,E., Swirskas,R.R., Weinburg,T. and Celniker,S.E.
Direct Submission
JOURNAL
TITLE
Submitted (23-APR-1999) Berkeley Drosophila Genome Project,
University of California Berkeley, Berkeley, CA 94720, USA
COMMENT
For further information about this sequence, including its location
and relationship to other sequences, please visit our web site
(http://fruitfly.berkeley.edu) or send email to
cdna@fruitfly.berkeley.edu
FEATURES
source
1. .2580
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1. .2580
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63. .2312
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Qy 1148 attatttcaaaaaa 1173
|||||
Db 577 ATTATTTCAAAAAA 1044 t

Query Match      2.2%; Score 26; DB 8; Length 602;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1148 attatttcaaaaaa 1173
|||||
Db 577 ATTATTTCAAAAAA 1044 t

RESULT 4
AF309947
LOCUS
DEFINITION
Dictyostelium discoideum Rac1A (rac1A) gene, complete cds; and
unknown gene.
ACCESSION
AF309947
VERSION
AF309947.1 GI:12007269
KEYWORDS
Dictyostelium discoideum.
SOURCE
Dictyostelium discoideum
ORGANISM
Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
REFERENCE
1 (bases 1 to 2518)
Rivero,F., Dislich,H., Glockner,G. and Noegel,A.A.
TITLE
The Dictyostelium discoideum family of Rho-related proteins
JOURNAL
Nucleic Acids Res. 29 (5), 1068-1079 (2001)
MEDLINE
21127961
REFERENCE
2 (bases 1 to 2518)
Rivero,F., Dislich,H. and Noegel,A.A.
AUTHORS
Direct Submission
TITLE
Submitted (28-SEP-2000) Institut fuer Biochemie I, Medizinische
Fakultaet, Universitaet zu Koeln, Joseph-Stelzmann-St. 52, Cologne
50931, Germany
FEATURES
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/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
join(83. .164,299. .356,501. .841,961. .1462)
/gene="rac1A"
/product="Rac1A"
83. .1462
/gene="rac1A"
join(350. .356,501. .841,961. .1197)
/gene="rac1A"
/codon_start=1
/product="Rac1A"
/protein_id="AAG45106.1"
/db_xref="GI:12007270"
/translation="MQAICVVVDGAVKTKLLISYTNNAFGVEYIPVFDNYGANY
MVDKGINGLMDTAQEDYDRPLSYPTQDVFLLCFISIPSPFNVGKWHPEIC
HAPNPVILVGTFLKMDREDKETQDRLEKKLYPISEYEQGLARKMEINAVKYLECAL
TQKGLTVDEARAVINPPLSKKKSSGCGNL"
misc_difference 1095
/gene="rac1A"
/note="compared to GenBank Accession Number L11588;
results in glutamate to glutamine substitution; Rac1B and
Rac1C also contain this substitution"
/replaces="c"
1335. .1340
/gene="rac1A"
/evidence=not_experimental
1382. .1387
/gene="rac1A"
/evidence=not_experimental
1424. .1429
/gene="rac1A"
/evidence=not_experimental
complement(join(1809. .2019,2120. .>2518))
/product="unknown"

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```

QY 1148 attatttcaaaaaaaaaaaaaaaaa 1173
|||||
Db 5549 ATTATTTCAAAAAAAAAAAAAAAA 5574

RESULT 7
PFPMAL4P1_0/c
WPCOMMENT
Sequence split into 4 fragments LOCUS PFMAL4P1 Accession AL034557
Fragment Name Begin End
PFMAL4P1_0 1 110000
PFMAL4P1_1 100001 210000
PFMAL4P1_2 200001 310000
PFMAL4P1_3 300001 392633
LOCUS PFMAL4P1 392633 bp DNA HTG 11-AUG-1999
DEFINITION Plasmodium falciparum chromosome 4 strain 3D7, *** SEQUENCING IN
PROGRESS ***; in unordered pieces.
ACCESSION AL034557.7 GI:5731897
VERSION AL034557.7
KEYWORDS HTG; HTGS-PHASE1.
SOURCE malaria parasite P. falciparum.
ORGANISM Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 392633)
AUTHORS Bowman,S., Churcher,C., Harris,B., Harris,D., Lawson,D., Quail,M.
and Barrell,B.
Direct Submission
TITLE Submitted (17-DEC-1998) P.falciparum Genome Sequencing Consortium,
JOURNAL The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CB10 1SA, UK
COMMENT
On Aug 12, 1999 this sequence version replaced gi:5531346.
For more information about this sequence or the Malaria Project,
see http://www.sanger.ac.uk/projects/P-falciparum. IMPORTANT: This
sequence is unfinished and does not necessarily represent the
correct sequence. Work on the sequence is in progress and the
release of this data is based on the understanding that the
sequence may change as work continues. The sequence may be
contaminated with foreign sequence from E.coli, Yeast, vector,
phage etc.
Order of segments is not known; 800 n's separate segments.
* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
FEATURES
source Location/Qualifiers
1..392633
/organism="Plasmodium falciparum"
/strain="3D7"
/db_xref="taxon:5833"
/chromosome="4"
BASE COUNT 146453 a 41490 c 42490 g 138992 t 23208 others
ORIGIN

Query Match 2.2%; Score 26; DB 2: Length 110000;
Best Local Similarity 100.0%; Pred. No. 0.026; 0; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 0;

QY 1148 attatttcaaaaaaaaaaaaaaaaa 1173
|||||
Db 6518 ATTATTTCAAAAAAAAAAAAAAAA 6493

RESULT 8
AC006280/c
LOCUS
DEFINITION AC006280 163443 bp DNA HTG 12-AUG-2000
Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN
PROGRESS ***; 1 ordered pieces.
ACCESSION AC006280
VERSION AC006280.8 GI:9797728
KEYWORDS HTG; HTGS-PHASE2.
SOURCE malaria parasite P. falciparum.

```



```

ORGANISM      Plasmodium falciparum
REFERENCE      Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
AUTHORS        1 (bases 1 to 163443)
                Hyman, R.W., Fung, E.L., Qin, F., Rowley, D., Mao, J., Tamaki, T.,
                Kurd, O.B., Conway, A.B. and Davis, R.W.
TITLE          Plasmodium falciparum 3D7 chromosome 12
JOURNAL         Unpublished
REFERENCE      2 (bases 1 to 163443)
                Hyman, R.W., Fung, E.L., Qin, F., Tamaki, T., Kurd, O.B. and Davis, R.W.
TITLE          Direct Submission
JOURNAL         Submitted (05-JAN-1999) Stanford DNA Sequencing and Technology
                Center, Stanford University, 855 California Avenue, Palo Alto, CA
                94304, USA
COMMENT        On Aug 12, 2000 this sequence version replaced gi:8810453.
                * NOTE: This is a 'working draft' sequence. It currently
                * consists of 1 contigs. Gaps between the contigs
                * are represented as runs of N. The order of the pieces
                * is believed to be correct as given, however the sizes
                * of the gaps between them are based on estimates that have
                * provided by the submitter.
                * This sequence will be replaced
                * by the finished sequence as soon as it is available and
                * the accession number will be preserved.
                * 1 163443: contig of 163443 bp in length.
FEATURES       Location/Qualifiers
                source
                1..163443
                /organism="Plasmodium falciparum"
                /db_xref="taxon:5833"
                /chromosome="12"
                /clone="PFYAC724"
                /clone="3D7"
BASE COUNT    65318 a 15421 c 17069 g 65635 t
ORIGIN
Query Match   2.2%; Score 26; DB 2; Length 163443;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attattcaaaaaaiaaaaaaaaaa 1173
|||||
Db 152102 ATTATTTCAAAAAAAAAAAAAAAAAA 152077

RESULT 9
AL590630      207596 bp      DNA      HTG      23-JUL-2001
DEFINITION    Mus musculus chromosome 8 clone RP23-353A15, *** SEQUENCING IN
PROGRESS ***, in unordered pieces.
ACCESSION     AL590630
VERSION       AL590630.12 GI:15026906
KEYWORDS      HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE        house mouse.
ORGANISM      Mus musculus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                1 (bases 1 to 207596)
REFERENCE      Direct Submission
AUTHORS        Submitted (22-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
TITLE          CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
JOURNAL        requests: clonerequest@sanger.ac.uk
COMMENT        On Jul 27, 2001 this sequence version replaced gi:15020764.
                ----- Genome Center
                Center: UK Medical Research Council
                Center code: UK-MRC
                Web site: http://mrcseq.har.mrc.ac.uk
                Contact: mouse@har.mrc.ac.uk
                ----- Project Information
                Center project name: BM353A15
                ----- Summary Statistics
                Assembly program: XGAP4; version 4.5
                Sequencing vector: plasmid; L08752; 100% of reads

```

```

Chemistry: Dye-terminator Big Dye; 98% of reads
Chemistry: Dye-primer Big Dye; 1% of reads
Consensus quality: 206899 bases at least Q40
Consensus quality: 207144 bases at least Q30
Consensus quality: 207339 bases at least Q20
Insert size: 207496; sum-of-contigs
Quality coverage: 8.40x in Q20 bases; agarose-fp
coverage: 9.96x in Q20 bases; agarose-fp

```

```

* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

```

FEATURES       Location/Qualifiers
                source
                1..207596
                /organism="Mus musculus"
                /db_xref="taxon:10090"
                /chromosome="8"
                /clone="RP23-353A15"
                /clone_lib="RPCI-23"
                1..107776
                /note="assembly-fragment:04776"
                misc_feature
                107877..207596
                /note="assembly-fragment:04821"
BASE COUNT    62985 a 41897 c 41972 g 60642 t 100 others
ORIGIN

```

```

Query Match   2.2%; Score 26; DB 2; Length 207596;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1148 attattcaaaaaaiaaaaaaaaaa 1173
|||||
Db 176615 ATTATTTCAAAAAAAAAAAAAAAAAA 176640

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```

RESULT 10
NTUPPGENE     1318 bp      mRNA      PLN      21-FEB-1997
LOCUS          N.tabacum mRNA for uracil phosphoribosyltransferase.
DEFINITION    Y11210
ACCESSION     Y11210
VERSION       Y11210.1 GI:1848213
KEYWORDS      phosphoribosyl transferase; upp gene.
SOURCE        common tobacco.
ORGANISM      Nicotiana tabacum
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                1 (bases 1 to 1318)
                Shen, W.H. and Gigot, C.
TITLE          Uracil phosphoribosyltransferase protein of Nicotiana tabacum
JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 1318)
AUTHORS        Shen, W.H.
TITLE          Direct Submission
JOURNAL        Submitted (13-FEB-1997) W.H. Shen, Institut de Biologie Moleculaire
                des Plantes, IBMP-CNRS, 12 rue du General Zimmer, 67084
                Strasbourg-cedex, FRANCE

```

```

FEATURES       Location/Qualifiers
                source
                1..1318
                /organism="Nicotiana tabacum"
                /strain="Bright yellow 2"
                /db_xref="taxon:4097"
                /dev_stage="S phase of the cell cycle"
                /tissue_type="synchronised cell suspension culture"
                /clone_lib="lambda ZAP Express BY2_S"
                /clone="53"
                90..764
                /gene="upp"
                90..764
                /gene="upp"

```

```

gene
CDS

```

```

/codon_start=1
/product="uracil phosphoribosyltransferase"
/protein_id="CAA72093.1"
/db_xref="GI:1848214"
/db_xref="SPTREMBL:P93394"
/translation="MAANKAMSGNMLVFPVPHPLIKHWSVLNEQTGPPCIPFNAM
SELGRLLYEASRDLPITGTSIQPMGVASVEFVDPREPVAIVPILRAGLALAFHAS
SILPATKTVHLGISNEETLOPSVYLNKLPDKPFGESRVIVVDPMLATGGTIVAAIDL
IKERGVDNSQIKVICAVGAPPALQKLEKFGPLGHVYAGILDPVTNDKGFIIPLGLDAG
DRSFGT"
polyA_site 1298
BASE COUNT 380 a 233 c 285 g 420 t
ORIGIN

Query Match 2.1%; Score 25; DB 8; Length 1318;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1149 ttattcaaaaaaaaaaaaaaaaa 1173
|||||
Db 1292 TTATTCAAAAAAAAAAAAAAAAAA 1316
|||||

RESULT 11
GGK60GENE 1445 bp mRNA VRT 01-JUN-1998
LOCUS Gallus gallus mRNA for K60 protein.
DEFINITION Y14971
ACCESSION Y14971
KEYWORDS K60 gene.
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 1445)
AUTHORS Sick,C.
TITLE Direct Submission
JOURNAL Submitted (21-AUG-1997) C. Sick, University of Freiburg, Department
of Virology, Hermann-Herder-Strasse 11, D-79008 Freiburg, FRG

REFERENCE 2 (bases 1 to 1445)
AUTHORS Sick,C.
JOURNAL Unpublished
FEATURES
source
1..1445
Location/Qualifiers
/organism="Gallus gallus"
/db_xref="taxon:9031"
/rearranged
/tissue_type="macrophage like"
/clone_lib="LPS stimulated HD-11 cells cloned in pcDNA1"
sig_peptide 246..305
CDS 246..560
/gene="k60"
/gene="k60"
/notes="LPS induced in primary macrophages, belongs to the
C-X-C chemokine family"
/codon_start=1
/product="K60 protein"
/protein_id="CAA75212.1"
/db_xref="GI:3175994"
/db_xref="SPTREMBL:O73912"
/translation="WMKAVAAVMALLTISMAGKMAQAARSAILRQCQIETHSKFI
HPKFIQNVLTSPGPHCKNVEIATLKDGREVCLODPTAPVVKLIKAILDKADTNKT
AS"
gene 246..560
/gene="k60"
mat_peptide 306..557
/gene="k60"
/gene="k60"
/product="K60 protein"
BASE COUNT 443 a 295 c 297 g 410 t
ORIGIN

```

```

Query Match 2.1%; Score 25; DB 5; Length 1445;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1149 ttattcaaaaaaaaaaaaaaaaa 1173
|||||
Db 1421 TTATTCAAAAAAAAAAAAAAAAAA 1445
|||||

RESULT 12
CEI9144 1498 bp DNA INV 21-JUN-2000
LOCUS Ceratitis capitata mssp-al gene for male specific serum polypeptide
alpha 1.
DEFINITION Y19144
ACCESSION Y19144
KEYWORDS Y19144.1 GI:6682266
SOURCE male specific serum polypeptide alpha 1; mssp-al gene.
ORGANISM Ceratitis capitata
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Tephritoidea; Tephritidae; Ceratitis.
REFERENCE 1 (bases 1 to 1498)
AUTHORS Christophides,G.K., Mintzas,A.C. and Komitopoulou,K.
TITLE Organization, evolution and expression of a multigene family
encoding putative members of the odourant binding protein family in
the medfly Ceratitis capitata
JOURNAL Insect Mol. Biol. 9 (2), 185-195 (2000)
MEDLINE 20225580
REFERENCE 2 (bases 1 to 1498)
AUTHORS Komitopoulou,K.S.
TITLE Direct Submission
JOURNAL Submitted (30-JUN-1999) K.S. Komitopoulou, University of Athens,
School of Biological Sciences, Panepistimiopolis, Kouponia 15701,
Athens, GREECE
FEATURES
source
1..1498
Location/Qualifiers
/organism="Ceratitis capitata"
/db_xref="taxon:7213"
TATA_signal 429..434
/gene="mssp-al"
gene 429..1430
/gene="mssp-al"
join(499..537,954..1349)
CDS /gene="mssp-al"
/codon_start=1
/product="male specific serum polypeptide alpha 1"
/protein_id="CAB64651.1"
/db_xref="GI:6682267"
/db_xref="SPTREMBL:Q9U3T0"
/translation="MKYFIVILAAVLAQAADDWVPKTPPEFNAIIRRECHKPEFSK
ELOKQEDNLDSDDETVRKVEVCVFRKWIIDAEDNFGRLVKQFQDAVLDEVENTIQ
KVNNCVDKNEQGSPIIDVYASRIQRCIDKTDIAPNLLKVIKGL"
499..537
/gene="mssp-al"
number=1
intron 538..953
/gene="mssp-al"
number=1
exon 954..1349
/gene="mssp-al"
number=2
polyA_signal 1425..1430
/gene="mssp-al"
BASE COUNT 549 a 228 c 292 g 429 t
ORIGIN

Query Match 2.1%; Score 25; DB 3; Length 1498;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1149 ttatttcaaaaaaaaaaaaaa 1173
Db 846 TTATTTCACAAAAA 870

RESULT 13
LOCUS CCA19145 1572 bp DNA INV 21-JUN-2000
DEFINITION Ceratitis capitata mssp-a2 gene for male specific serum polypeptide
alpha 2.
ACCESSION Y19145
VERSION Y19145.1 GI:6682268
KEYWORDS male specific serum polypeptide alpha 2; mssp-a2 gene.
SOURCE Mediterranean fruit fly.
ORGANISM Ceratitis capitata
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Tephritoidea; Tephritidae; Ceratitis.
REFERENCE 1 (bases 1 to 1572)
AUTHORS Christophides G.K., Mintzas A.C. and Komitopoulou K.
TITLE Organization, evolution and expression of a multigene family
encoding putative members of the odourant binding protein family in
the medfly Ceratitis capitata
JOURNAL Insect Mol. Biol. 9 (2), 185-195 (2000)
MEDLINE 20225580
REFERENCE 2 (bases 1 to 1572)
AUTHORS Komitopoulou K.S.
TITLE Direct Submission
JOURNAL Submitted (30-JUN-1999) K.S. Komitopoulou, University of Athens,
School of Biological Sciences, Panepistimiopolis, Kouponia 15701,
Athens, GREECE

FEATURES
source Location/Qualifiers
1. 1572
/organism="Ceratitis capitata"
/db_xref="taxon:7213"
/tissue_type="fat body"
492..497
/gene="mssp-a2"
492..1504
/gene="mssp-a2"
join(562..600,1028..1423)
/gene="mssp-a2"
/codon_start=1
/product="male specific serum polypeptide alpha 2"
/protein_id="CA864445.1"
/db_xref="GI:6682269"
/db_xref="SPTREMBL:Q9U3T9"
/translation="MKYFIVILAAVLAQAADDWPKTPPEFNIRRECHKEFPFSK
ELQKQEEIDFSDTEVRKYEVCFRKWGIIDADDTFHGERLVKQFEAVLDGVEGIEQ
KVNCVKNEQSGPIDVYASRIQQCDIKTDIAPKLLKVLKGL"
562..600
/gene="mssp-a2"
/number=1
601..1027
/gene="mssp-a2"
/number=1
1028..1423
/gene="mssp-a2"
/number=2
1499..1504
/gene="mssp-a2"
443 t
BASE COUNT 596 a 235 c 298 g 443 t
ORIGIN

Query Match 2.1%; Score 25; DB 3; Length 1572;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaa 1173
Db 913 TTATTTCACAAAAA 937

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RESULT 14
LOCUS AK026358 1633 bp mRNA PRI 29-SEP-2000
DEFINITION Homo sapiens cDNA: FLJ22705 fis, clone HSI13142.
ACCESSION AK026358
VERSION AK026358.1 GI:10439199
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens human small intestine cDNA to mRNA, clone_lib:HSI
clone:HSI13142.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Kawabata A., Hiki J., Kobatake N., Inagaki H., Ikema Y.,
Okamoto S., Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T.,
Shibahara T., Tanaka T., Nakamura Y., Isogai T. and Sugano S.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished (2000)
REFERENCE 2 (bases 1 to 1633)
AUTHORS Sugano S., Suzuki Y., Ota T., Obayashi M., Nishi T., Isogai T.,
Shibahara T., Tanaka T. and Nakamura Y.
TITLE Direct Submission
JOURNAL Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sumio
Sugano, Institute of Medical Science, University of Tokyo,
Laboratory of Genome Structure Analysis, Human Genome Center;
Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail:cdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing; Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing; Department of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).
FEATURES
source Location/Qualifiers
1. 1633
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HSI13142"
/clone_lib="HSI"
/tissue_type="human small intestine"
/note="cloning vector pME18SFL3"
543 a 241 c 272 g 577 t
BASE COUNT 543 a 241 c 272 g 577 t
ORIGIN

Query Match 2.1%; Score 25; DB 9; Length 1633;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attattcaaaaaaaaaaaaaa 1172
Db 1609 ATTATTTCACAAAAA 1633

RESULT 15
LOCUS AF057693 1683 bp mRNA INV 19-JUN-2001
DEFINITION Sacculina carcini engrailed-a homeobox protein (en-a) mRNA,
en-a-E20 allele, complete cds.
ACCESSION AF057693
VERSION AF057693.1 GI:3746523
KEYWORDS Sacculina carcini.
ORGANISM Sacculina carcini
Eukaryota; Metazoa; Arthropoda; Crustacea; Maxillopoda; Cirripedia;
Rhizocephala; Kentrogonida; Sacculinidae; Sacculina.
REFERENCE 1 (bases 1 to 1683)
AUTHORS Queinnee E., Mouchel-Vielh E., Guimonneau M., Gibert J.M.,
Turquier Y. and Deutsch J.S.
TITLE Cloning and expression of the engrailed.a gene of the barnacle

```

```

CDS
join(101..391,776..930,1040..1637)
/gene="G alpha 5"
/codon_start=1
/product="guanine nucleotide-binding protein alpha subunit
5"
/protein_id="AAB04097.1"
/db_xref="GI:687741"
/translation="MGCILTIETIAKRSRDIDYOLRKEEGSKNETKLLLLGPGESGKSTI
FKMKIIOQDGFSIDERLEYRIIYGNCSIQMKVLTAAISQDLKPNPNDNETREFEK
FSKIPGNSWTLAETADIKQIWSDDQNIYMKDKFYOLNDSAAFYDNIDNIRFANE
NYVPQDDVLRGRVTTGTQEAEHFKFINIEFRLMDVGQGRSRRRWIHCDFSVAVIF
CVVLESDYQTLREESONRMKESLMLFDEIVNSHMFNTAFIIFENKVLDFREKIARI
DLGDVEPAYTGLGSFSDNSTQFIKKKFLDLSCTGNQRIFAHFTCAIDTANTIQFVFEHVA
TLLKNFIENIINY"
intron 392..775
exon 776..930
/gene="G alpha 5"
intron 931..1039
exon 1040..1639
3'UTR 1638..1639
BASE COUNT 661 a 185 c 213 g 646 t
ORIGIN
Query Match 2.1%; Score 25; DB 3; Length 1705;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 1672 TTATTTCAAAAAAAAAAAAAAAAAA 1648

RESULT 17
OV15993
LOCUS OV15993 1891 bp mRNA INV 28-DEC-1997
DEFINITION Onchocerca volvulus mRNA for novel antigen, clone OV-47.
ACCESSION Y15993
VERSION Y15993.1 GI:2739313
KEYWORDS antigen.
SOURCE Onchocerca volvulus.
ORGANISM Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidae;
Onchocercidae; Onchocerca.
1 (bases 1 to 1891)
Titanji,V.P.K., Sakwe,A.M., Ghogomu,S.M., Souopgui,J., Djokam,R.T.,
Perler,F. and Rask,L.
P1
A cDNA coding for a novel antigen from Onchocerca volvulus
Unpublished
2 (bases 1 to 1891)
Sakwe,A.
Direct Submission
Submitted (19-DEC-1997) A. Sakwe, Biotechnology Centre, University
of Yaounde, Department of Life Sciences, Faculty of Science,
University of Buera, P.O. Box 63, Buena, CAMEROON
The clone was selected by screening an Onchocerca volvulus lambda
gt11 expression cDNA library prepared from adult female worms
(Francine
Perler, unpublished) using a rabbit antiserum to the adult female
surface
proteins. This antiserum which recognised about a dozen O. volvulus
polypeptides was shown to be active in mediating leucocyte
adherence and
cytotoxicity to O. volvulus microfilariae. The product of the cloned
gene has
been expressed in E.coli and found to react strongly with
oncocercaiasis
patient serum pools from patients with varying skin microfilaria
density.
Location/Qualifiers
1..1891
/organism="Onchocerca volvulus"
/strain="Forest"

FEATURES
source

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```

/db_xref="taxon:6282"
/sex="female"
/clone_lib="lambda gt11"
/clone="OV-47"
/dev_stage="adult"
10..1089
/codon_start=1
/product="antigen"
/protein_id="CAA75924.1"
/db_xref="GI:2739314"
/db_xref="SPTREMBL:O46146"
/translation="MSHYLSIYNLSHLLIKLIYCIILQSQALRINTGTSRRNQPS
ILAKFGQIDPLDAEHSRGEVYGNVSPPIINGARGVLLIVPKTLVNGFLNKATLEOS
CDSLQTSSTLAFACELSDGKDDVMRIPCPAGKLCVEEDMEKVINDSOMTLRIEE
PSAPQWYVIVACVLDTHCLWKSVRKEVIVHYDLWTNGSPLMHYLNPFYQFSFEE
ONSARIYMLFILIYVGFQCOMRSVMLCNSASFFRHOLLNCIIVLTKFTGLTLCLNV
ITFSDGGGILFARLLGELIARLMTCLLCLLILLYSGWSFGNSSEILLIYPKVVIWG
LITSARHFLUFFINLHSLHLHTIIC"
1858
polya_site
BASE COUNT 509 a 306 c 366 g 710 t
ORIGIN

Query Match 2.1%; Score 25; DB 3; Length 1891;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 1852 TTATTTCACAAAAA 1876

RESULT 18
XLU59483
LOCUS
DEFINITION Xenopus laevis putative transcription factor VegT (VegT) mRNA,
complete cds.
ACCESSION U59483
VERSION U59483.1
KEYWORDS GI:2725622
SOURCE African clawed frog.
ORGANISM
Xenopus laevis
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 2691)
Zhang, J. and King, M.L.
Xenopus VegT RNA is localized to the vegetal cortex during
oogenesis and encodes a novel T-box transcription factor involved
in mesodermal patterning
Development 122 (12), 4119-4129 (1996)
97164724
2 (bases 1 to 2691)
Zhang, J. and King, M.L.
Direct Submission
Submitted (29-MAY-1996) Department of Cell Biology and Anatomy
(R-124), University of Miami School of Medicine, 1600 NW 10 Avenue,
Miami, FL 33101, USA
On Dec 29, 1997 this sequence version replaced gi:1698557.
FEATURES
source
1..2691
/organism="Xenopus laevis"
/db_xref="taxon:8355"
1..2691
/gene="VegT"
/notes="vegetally localized mRNA"
57..1424
/gene="VegT"
/notes="putative transcription factor"
/codon_start=1
/product="vegT"
/protein_id="AAB93301.1"
/db_xref="GI:2725623"

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/translation="MRNCRCEGLSAGHLEPEASNCASDVKSSPDMDSVSSQDSLYL
PNTVGASLEDQDLWSQFHQEGTEMIITKSGRMFPQCKIRLFGHPYAKYMLLVDFVP
LDNFRYKWNKNQWEAAAGKAPPCRTYVHPDSPAPGAHMKDPCICFKLKTNTILD
QOQHILHSMHRYKPRFHVQSDMYNSPWGLVQVFSFETFTSVAYQNEKITLKL
INHPFAKGFREOERSHRRDDVLKILQOSPSKRQKKWEDSPADISDFPKAICVKE
ESTMDPAGYQNWVSDHEANQGLTSPSEGANQOQVPTSSNFYKSHYRRSSOH
LSSPFELGEPSSRLTPDIATVPDSDPLAVFHVPTQNSAPERTCSMNFWEAPMK
QPLRGAMYSPYAGDQWLVAQOQYRPVGYTAYPTDLSTOGAVAHPHSANDWSQYSLF
PYSCW"
BASE COUNT 753 a 574 c 612 g 752 t
ORIGIN

Query Match 2.1%; Score 25; DB 5; Length 2691;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 2656 TTATTTCACAAAAA 2680

RESULT 19
XLU89707
LOCUS
DEFINITION Xenopus laevis Brachyury and Tbx related protein (Brat) mRNA,
complete cds.
ACCESSION U89707
VERSION U89707.1
KEYWORDS GI:1881739
SOURCE African clawed frog.
ORGANISM
Xenopus laevis
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 2703)
Horb, M.E. and Thomsen, G.H.
A vegetally-localized T-box transcription factor in Xenopus eggs
specifies mesoderm and endoderm and is essential for embryonic
mesoderm formation
Development (1997) In press
2 (bases 1 to 2703)
Horb, M.E. and Thomsen, G.H.
Direct Submission
Submitted (14-FEB-1997) Biochemistry and Cell Biology, SUNY at
Stony Brook, Life Sciences 338, Stony Brook, NY 11794-5215, USA
LOCATION/Qualifiers
1..2703
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/dev_stage="stage 10.5 gastrula"
/tissue_type="ventral mesoderm/endoderm"
1..2703
/gene="Brat"
80..1447
/gene="Brat"
/function="transcriptional activator"
/notes="T-box transcription factor; similar to Antipodean
encoded by GenBank Accession Number X99905 and Veg-T
encoded by GenBank Accession Number U59483"
/codon_start=1
/product="Brachyury and Tbx related protein"
/protein_id="AAB49478.1"
/db_xref="GI:1881740"
/translation="MRNCRCEGLSAGHLEPEASNCASDVKSSPDMDSVSSQDSLYL
PNTVGASLEDQDLWSQFHQEGTEMIITKSGRMFPQCKIRLFGHPYAKYMLLVDFVP
LDNFRYKWNKNQWEAAAGKAPPCRTYVHPDSPAPGAHMKDPCICFKLKTNTILD
QOQHILHSMHRYKPRFHVQSDMYNSPWGLVQVFSFETFTSVAYQNEKITLKL
INHPFAKGFREOERSHRRDDVLKILQOSPSKRQKKWEDSPADISDFPKAICVKE
ESTMDPAGYQNWVSDHEANQGLTSPSEGANQOQVPTSSNFYKSHYRRSSOH
LSSPFELGEPSSRLTPDIATVPDSDPLAVFHVPTQNSAPERTCSMNFWEAPMK
QPLRGAMYSPYAGDQWLVAQOQYRPVGYTAYPTDLSTOGAVAHPHSANDWSQYSLF
PYSCW"

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BASE COUNT      747 a   583 c   617 g   756 t
ORIGIN
Query Match
Best Local Similarity 100.0%; DB 5; Length 2703;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 2679 TTATTTCACAAAAAAAAAAAAAAAAA 2703

RESULT 20
AF083225 2771 bp mRNA INV 11-MAR-1999
LOCUS Caenorhabditis elegans nuclear receptor NHR-7 (nhr-7) mRNA,
DEFINITION complete cds.
ACCESSION AF083225
VERSION AF083225.1 GI:4139075
KEYWORDS Caenorhabditis elegans.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans
REFERENCE 1 (bases 1 to 2771)
AUTHORS Sluder, A.E., Mathews, S.W., Hough, D., Yin, V.P., and Maina, C.V.
TITLE The nuclear receptor superfamily has undergone extensive
proliferation and diversification in nematodes
JOURNAL Genome Res. 9 (2), 103-120 (1999)
MEDLINE 99148134
REFERENCE 2 (bases 1 to 2771)
AUTHORS Sluder, A.E., Mathews, S.W., Yin, V.P., Hough, D. and Maina, C.V.
TITLE Direct Submission
JOURNAL Submitted (10-AUG-1998) New England Biolabs, 32 Tozer Rd., Beverly,
MA 01915, USA

FEATURES
source
location/Qualifiers
1..2771
/organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
/chromosome="IV"
/clone="Y72H7; Y51B3; Y37G7"
/notes="partial sequence obtained from EST clone yk396h7"
gene 1..2771
/gene="nhr-7"
CDS 1115..2725
/codon_start=1
/product="nuclear receptor NHR-7"
/protein_id="AAD03683.1"
/db_xref="GI:4139076"
/translation="MGSYTRNICAVGDPAPKIHGYVLACFCCKGFFRRVAVKDGGRNKY
VCFERKCEVTFERNACRYCFRKLCLVGMNPDYVRDREKSKGKTVLKKKSVSR
SUSYRLADPSDTLSLSPSRKQLSEIGKLAETCTSTNFDGIGNFLSKLIADRSAL
RKTGDSFAMDCNSPRLNQELGIERIVQCVDYIDRLVLMLEERHCKFSVEDKSL
ISDTMIHLLEFSTRFVAKGAPGLDLKLSLAQLPCTHTLTOKIADVFETYLKRP
STIEYSLKAYIVLSAESVLSNLSLSLARENLSELLFPKVIKSRNKTSGISRANS
LSYLLHFVYESNLSARIKRSQPFVRDSDPKIFPHKILITDIINPEVSDLLTTANC
RLKLTQMGSSLSVPVPPSDTVLPHFSPSLSPQISAPPPPOQOQYDYSQMPST
SYTPANSPSPQSPRPNLSLSPKIPLEMTKSIIEFLRPNGMTTDEMKNKPLEKNWADG
FRLTPVFNKDIYSQFFPELSLNQHHPF"
BASE COUNT      881 a   559 c   423 g   908 t
ORIGIN
Query Match
Best Local Similarity 100.0%; DB 3; Length 2771;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 2747 TTATTTCACAAAAAAAAAAAAAAAAA 2771

RESULT 21
PPRESAGI 3268 bp DNA INV 26-APR-1991
LOCUS P.falciiparum FC27 RESA gene for ring-infected erythrocyte surface
DEFINITION antigen.
ACCESSION X04572
VERSION X04572.1 GI:9960
KEYWORDS antigen; ring-infected erythrocyte surface antigen; surface
antigen.
SOURCE malaria parasite P. falciiparum.
ORGANISM Plasmodium falciiparum
REFERENCE 1 (bases 1 to 3268)
AUTHORS Favaloro, J.M., Coppel, R.L., Corcoran, L.M., Foote, S.J., Brown, G.V.,
Anders, R.F. and Kemp, D.J.
TITLE Structure of the RESA gene of plasmodium falciiparum
JOURNAL Nucleic Acids Res. 14 (21), 8265-8277 (1986)
MEDLINE 87066710
COMMENT For 3' FC27 cDNA sequence see X05182, for overlapping NF7 cDNA
sequence see X05181
Data kindly reviewed (10-JUL-1987) by Favaloro J.

FEATURES
source
location/Qualifiers
1..3268
/organism="Plasmodium falciiparum"
/strain="FC27 (FCQ27/PNG Papua New Guinea isolate)"
/db_xref="taxon:5833"
/join(801..995,1199..3268)
/codon_start=1
/product="ring-infected erythrocyte surface antigen"
/protein_id="CAA28241.1"
/db_xref="GI:9961"
/db_xref="SWISS-PROT:P13830"
/translation="MRPHAYSWIFSSQYMGTKNVKKNPTIYSPDDEKKNENKSF
KVLCKRGVLPIGLIYLILNGLNGSSSGVQFTDRGRNLYGETLPVNPVADSE
FNVVSVQVGLPFPEKFTLESPPDIDHTNLGFKNEKFTMDVNRYSNNYEALPHIS
EPFLIVDKVLFDYNEKVDNLGRSGGDIKKMQTLWDEIMDKRKYDSLKEKQKTY
SQYKQVMPKEAVESKWTQCIKILDOGGENLEERLNSQPKWYKQYLNLEEVRLTY
VLNOIAKALSNQIYQSCRKIMNSDISSFKHINELKSLERHAAKAAEAMKKRAQKPK
KKSRGWLCCGGGDIETVEPQEPVQVQEQVNYGDLPLSLASITNSAINIYD
TVKGVGDLHETSADALYDELLDFDLKQYMDLDTSEESVEEENEEHTVDDEHVE
EHTADDEHVEETVADEHVEETVADEHVEETVADEHVEETVADEHVEETVADEHVE
QTSAAATIEIDTLIYDILGVNADNMEITERFKLAENYIYQSGSTVFHNFKR
VNEAYQVLGDIIDKKRWYKYGDIKQVNFMPNPSIFVLLSLEKFKDFTGTPQITVTL
RFFFEKLSMNDLENSEHLLKFMQYQKREAHVSEYLLNLOPCQIAGDSKNVPII
TKLELKGSRFDIPILESRLWIFKHVAKTHLKSSKSAKKLQQTQANKQELANINN
LMSTLKEVLGSSEQ"
801..995
/product="put. signal peptide"
996..1198
/note="intron I"
2309..2515
/note="repetitious region 1"
BASE COUNT      1339 a   353 c   444 g   1132 t
ORIGIN
sig_peptide
intron
misc_feature
BASE COUNT      1339 a   353 c   444 g   1132 t
ORIGIN
Query Match
Best Local Similarity 100.0%; DB 3; Length 3268;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 1030 TTATTTCACAAAAAAAAAAAAAAAAA 1006

RESULT 22
A00661/c 4591 bp DNA PAT 09-JUL-1993
LOCUS P.falciiparum RESA gene for ring-infected erythrocyte surface
DEFINITION antigen.
ACCESSION A00661
VERSION A00661.1 GI:410747

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KEYWORDS
SOURCE      malaria parasite P. falciparum.
ORGANISM    Plasmodium falciparum
REFERENCE   1 (bases 1 to 4591)
AUTHORS     ANTIGENS OF PLASMODIUM FALCIPARUM
TITLE       Patent: WO 8601802-A 1 27-MAR-1986;
JOURNAL
FEATURES
  source    1..4591
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            /db_xref="taxon:5833"
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            join(801..995,1199..4225)
            /gene="RESA"
            /codon_start=1
            /product="ring-infested erythrocyte surface antigen"
            /protein_id="CAA00077.1"
            /db_xref="GI:410748"
            /translation="MRPFAYSHIFSQYQMGTKNVEKKNPTIYFDDDEKRNENKSF
            KVLCSRGVLPITGILFIILNGLNGSSGQFTDRCSRNLVGETLPVPYADSE
            NPVSVQFLPPEKFTFLESPPDIDHTNIGLFNEKFMFDVNRYSYNYEALPHIS
            EFNPLVDKVLFDYNEKVDNLSRGGDIKKQTLWDEIMDKRKYDSLKELOKTY
            SQYKVDMPKEAYESKWTQCILIDOGGENLEERLNSQFNWYRKYLNLEKRLT
            VLNOIAWKALSNIOYSCRKIMNSDISFKHINELKSLFRAKAAEAEMKRAQPK
            KKSRRGCLCCGGDIETVEPQOEVPQVQEQVNEYGDILPSLRASINSAINPY
            TVDGYVLUHETSDALYDEDLFLDLKQKMDLDTSEESVEENEHEHTVDDERH
            EHTADDEHEEPTVADEHEEPTVADEHEEPTVADEHEEPTVADEHEEPTVADE
            QTSAAPTIETDLYLIGVGNADMEITERFKLAENYYPQSRSGTVFHNFRK
            VNEAYQVLGIDDKRWYKYGVDIKQVFNMPISFYLLSSLEKPKDFTGTQIVTLL
            RFFLEKRLSNDELKSEHLKPFMEQYQKREAHVSEYLLNLIQPCIAGDSKNWPII
            TKLEGLKSGRDFPILESRLWLFKVAKTHLKSSKSAKLOQTOANKQELANINN
            LNSTLEYLSSQMSIYINENINSYNDNGNSKISDLSITDQKEILEKIVITIV
            DISLYDIENALNAASQLLSDNSVDEKTLKRAQSLKLUSSIMERYAGGKRNDKSKN
            FDTKLVIGYIMHGISTINTEMKNQENVEPHVOHNAENVEHDAENVEHDAENVEH
            DAENVEHDAENVEENVEENVEENVEENVEENVEENVEENVEENVEENVEENVEE
            NVEENVEENVEENVEENVEENVEENVEENVEENVEENVEENVEENVEENVEE
            EVEENVEENVEENVEENVEENVEENVEENVEENVEENVEENVEENVEENVEE
            <801..995
            /gene="RESA"
            /number=1
            996..1198
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            /number=1
            1199..>4225
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            /number=2
            BASE COUNT  1933 a  438 c  673 g  1547 t
            ORIGIN
            Query Match      2.1%; Score 25; DB 6; Length 4591;
            Best Local Similarity 100.0%; Pred. No. 0.14;
            Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
            Oy  1149 ttattcaaaaaaaaaaaaaaaaaa 1173
                |||||
            Db  1030 TTATTTCAAAAAAAAAAAAAAAAAA 1006
                |||||
            RESULT 23
            AC004631
            LOCUS      20413 bp  DNA  PRI  30-APR-1998
            DEFINITION Homo sapiens chromosome 5, PAC clone 154d1 (LBNL H113), complete
            sequence.
            ACCESSION  AC004631 AC002184
            VERSION     AC004631.1 GI:3094997
            KEYWORDS    HTG.
            SOURCE      human.
            ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE   1 (bases 1 to 20413)
AUTHORS     Kimmerly, W., Bondoc, M., Cheng, J., Connolly, K.S., Gunning, K.M.,
            Kadner, K., Miguel, T., Miller, C., Pitluck, S., Pollard, M.,
            Rojeski, H., Subramanian, S. and Martin, C.H.
            Sequencing of human chromosome 5
            Unpublished
            2 (bases 1 to 20413)
            Rieke, D.O.
            Large Scale Sequence Analysis and Annotation with the Sequence
            Comparison Analysis (SCAN) System
            Unpublished
            3 (bases 1 to 20413)
            Kimmerly, W., Bondoc, M., Cheng, J., Connolly, K.S., Gunning, K.M.,
            Kadner, K., Miguel, T., Miller, C., Pitluck, S., Pollard, M.,
            Rojeski, H., Subramanian, S. and Martin, C.H.
            Direct Submission
            Submitted (30-APR-1998) Human Genome Center, DOE Joint Genome
            Institute, Lawrence Berkeley National Laboratory, MS 74-157,
            Berkeley, CA 94720, U.S.A.
            Sequence submitted by:
            DOE Joint Genome Institute.
            Location/Qualifiers
              source      1..20413
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /map="5q"
                        /clone="154d1"
                        /chromosome="5"
                        /note="LBNL H113"
                        243..342
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                        398..731
                        /rpt_family="AluSx"
                        705..732
                        /note="(AAA)7"
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                        /rpt_unit=AAAG
                        complement(775..1095)
                        /rpt_family="Alu"
                        1138..1284
                        /rpt_family="MLT1a"
                        2515..2536
                        /note="(A)22"
                        /rpt_type=tandem
                        /rpt_unit=A
                        complement(2624..2805)
                        /rpt_family="MLT1P"
                        /note="GATL 2 excellent exon, frame 0"
                        5356..5647
                        /rpt_family="Alu"
                        7835..8143
                        /rpt_family="Alu"
                        complement(9100..9159)
                        /rpt_family="Alu"
                        9372..9563
                        /rpt_family="Alu"
                        10472..10773
                        /rpt_family="Alu"
                        10752..10771
                        /note="(A)20"
                        /rpt_type=tandem
                        /rpt_unit=A
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                        /rpt_family="L1"
                        11237..11310
                        /rpt_family="L1ME"
                        complement(11586..11869)
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                        complement(12028..12162)
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12291..12597
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12593..13092
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13163..13469
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13465..13595
repeat_region      /rpt_family="L1MB3"
complement(14012..14151)
repeat_region      /rpt_family="Alu"
14178..14470
repeat_region      /rpt_family="Alu"
complement(14691..14729)
misc_feature       /note="GRAL1 2 excellent exon, frame 0"
14763..14818
repeat_region      /rpt_family="MIR"
15023..15163
misc_feature       /note="51% protein identity HLA-DR B protein precursor"
15101..15564
repeat_region      /rpt_family="Alu"
15243..15386
repeat_region      /rpt_family="L1"
17769..17858
repeat_region      /rpt_family="Alu"
17841..17860
repeat_region      /note="(A)20"
/rpt_type=tandem
/rpt_unit=A
repeat_region      /rpt_family="Alu"
17870..18152
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18175..18202
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/rpt_type=tandem
/rpt_unit=AGG
repeat_region      /rpt_family="Alu"
19053..19350
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5568 a 4820 c 5355 g 4670 t

BASE COUNT 5568 a 4820 c 5355 g 4670 t
ORIGIN

Query Match      2.1%; Score 25; DB 9; Length 20413;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 2508 TTATTTCAAAAAAAAAAAAAAAAAA 2532

RESULT 24
AC014449 AC014449 25147 bp DNA HTG 16-NOV-1999
LOCUS Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
DEFINITION pieces.
ACCESSION AC014449
VERSION AC014449.1 GI:6436886
KEYWORDS HTG; HTGS_PHASE2.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 25147)
AUTHORS Adams,M. and Venter,J.C.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
COMMENT This sequence was identified as CD1:10212978 by the submitter.
For further information on this sequence e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and

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FEATURES
source
1..25147
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"

BASE COUNT 6651 a 5450 c 5655 g 7391 t
ORIGIN

Query Match      2.1%; Score 25; DB 2; Length 25147;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 19342 TTATTTCAAAAAAAAAAAAAAAAAA 19366

RESULT 25
AC006540 AC006540 34000 bp DNA PRI 28-JUL-2000
LOCUS Homo sapiens chromosome 19, cosmid F23842, complete sequence.
DEFINITION AC006540
ACCESSION AC006540
VERSION AC006540.2 GI:9558586
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 34000)
AUTHORS Lamerdin,J.E., McGready,P.M., Skowronski,E., Viswanathan,V.,
Burkhardt-Schultz,K.J., Gordon,L., Dias,J., Ramirez,M.,
Stilwagen,S., Phan,H., Velasco,N., Do,L., Regala,W., Terry,A.,
Garnes,J., Dancanap,L., Erler,A., Christensen,M., Georgescu,A.,
Avila,J., Lib,S., Attix,C., Andreise,T., Frankheim,M.,
Amico-Keller,G., Coefield,J., Duarte,S., Lucas,S., Bruce,R.,
Thomas,P., Quan,G., Kronmiller,B., Arellano,A., Brower,A.,
Sanders,C., Ow,D., Nolan,M., Trong,S., Kobayashi,A., Olsen,A.S. and
Carrano,A.V.
TITLE Sequence analysis of a 1.9 Mb region in 19q13.2 between APOE and
D19S412
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 34000)
AUTHORS Lamerdin,J.E.
TITLE Direct Submission
JOURNAL Submitted (07-FEB-1999) Joint Genome Institute, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
REFERENCE 3 (bases 1 to 34000)
AUTHORS Lamerdin,J.E.
TITLE Direct Submission
JOURNAL Submitted (28-JUL-2000) DOE Joint Genome Institute, Lawrence
Livermore National Laboratory, Livermore, CA 94550
COMMENT On Jul 28, 2000 this sequence version replaced gi:4235139.
Map and sequence are oriented from centromere to q-telomere. This
accession represents bases 1 to 34,000 of the cosmid F23842. Insert.
Cosmid F23842 (L1NLF-197C2) is overlapped on the left by BC34685.
(CTB-14D10, AC008623) from bases 1 to 18,432 of this accession, and
overlaps cosmid R30477 (L1NLF-266D1, AC011545) on the right from
bases 30,197 to 34,000 of this accession.
FEATURES
source
1..34000
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
/map="19q13.2 between APOE and D19S412"
/clone="F23842"
/cell_line="UV5HL9-5B"
/clone_lib="L19NC02 F chromosome 19-specific cosmid
library"
/note="Cosmid library constructed at LLNL from flow-sorted
chromosomes from hybrid UV5HL9-5B, which carries
chromosome 19 as its only human chromosome."
misc_feature 28..833

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* the accession number will be preserved.


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/note="DDS similarity to overlapping ESTs:
(388..28) R85163 y043b05.r1 Homo sapiens cDNA clone 180657
5'; (1..362) 98% identity.
(337..833) R55694 y988f12.r1 Homo sapiens cDNA clone 40397
5'; (1..517) 90% identity.
177..261
/note="predicted exon, program: grrail2exons_human_1.3,
frame: 2, quality: excellent, score: 75.000"
complement(1178..1613)
/note="DDS similarity to R55695 y988f12.s1 Homo sapiens
cDNA clone 40397 3'; (1..439) 98% identity."
1566..1646
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complement(join(1633..3065,15899..16065,23127..23271))
/product="Human putative astrocytic NOVA-like RNA-binding
protein (ANOVA) mRNA, partial cds"
1906..1967
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complement(join(1983..3065,15899..16065,23127..23271))
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sapiens]"
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/translation="EECEYFLKVLIPSYAAGSLIIGKGGTIVLOKETGATIKLSKS
DEYPTGTERVCLVQGTAEALNAVHPIAEKVRIPQAMTKPEVINLIQPTMTNPDRA
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VHRAASVAGLVQGVQSSCLNIPYANVAGPVANSPTGSPYSPADVLPAANAASA
AASGLGTPAGLVAGFAAPAFSGTDLLAISTALNTIASYNTNSLIGLNSAA
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NGYLGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
ILGKGGKTLVEYQELTGARIQISKKEFLPGTNRNRTVITGSPATQAAYLLISQV
YEGVGRASNPQKVG"
complement(2257..2373)
/rpt_family="(CGG)n"
2413..2534
/rpt_family="(CGG)n"
2711..2820
/rpt_family="(CGG)n"
2734..3065
/note="DDS similarity to Overlapping ESTs:
(3065..2734) AA904538 ok08f03.s1 Soares NFL_T_GBC_S1 Homo
sapiens cDNA clone IMAGE:1507229 3', similar to
SW:NOAL_HUMAN P51513 ONCONEURAL VENTRAL ANTIGEN-1 ;
(331..1) 99% identity.
(2735..3091) AI077966 oy39c05.s1
Soares parathyroid tumor NbHPA Homo sapiens cDNA clone
IMAGE:1668200 3', similar to SW:NOAL_HUMAN P51513
ONCONEURAL VENTRAL ANTIGEN-1 ; (1..356) 97% identity.
(3065..2736) W35411 zc08e08.s1 Soares parathyroid tumor
NbHPA Homo sapiens cDNA clone 321734 3', similar to
PIR:A53184 A53184 myc
far upstream element-binding protein - human ; (328..1)
96% identity.
(3065..2752) AI040329 oy33b05.x1 Soares parathyroid_t
umor NbHPA Homo sapiens cDNA clone IMAGE:1667601 3',
similar to SW:NOAL_HUM
AN P51513 ONCONEURAL VENTRAL ANTIGEN-1 ; (314..1) 99%
identity.
and others."
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/rpt_family="AT-rich"
3128..3430
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/rpt_family="AluJo"
3735..3861
/rpt_family="FLAM_C"
complement(4122..4193)
/rpt_family="MIR"
4271..4644
/rpt_family="MLT1B"

repeat_region 5048..5170
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6988..7101
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8065..8141
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8712..9011
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13762..13918
/rpt_family="AluJb"
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complement(14297..14484)
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/note="BLASTN similarity to z57045 (84. .232); match: 0.99,

Query Match

Best Local Similarity 2.1%; Score 25; DB 9; Length 34000;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1149 ttatttcaaaaaa1173

Db 11435 TTATTTCAAAAA11459

RESULT 26

AC034287 43324 bp DNA HTG 26-FEB-2001
Mus musculus chromosome 11 clone RP23-239L6 map 11, LOW-PASS
SEQUENCE SAMPLING.
AC034287
AC034287.3 GI:13123926
HTG; HTGS_PHASE0.
SOURCE house mouse.
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 43324)

Authors Birren, B., Linton, L., Nusbaum, C., and Lander, E.

Title Mus musculus chromosome 11, clone RP23-239L6

JOURNAL

REFERENCE

2 (bases 1 to 43324)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G.,
Campiano, A., Castle, A., Choquel, Y., Collangelo, M., Collins, S.,
Collamore, A., Cooke, P., DeArelano, K., Dewar, K., Diaz, J.S.,
Dodge, S., Domino, M., Doyle, S., Goyette, P., FitzHugh, W., Gage, D.,
Galaad, J., Gardyna, S., Ginde, S., Goyette, P., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Hearford, A., Horton, L.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRoque, K., Lamazares, R., Landers, T., Lehotzky, J.,
Levine, R., Liu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
Meldrum, J., Meneus, L., Mihova, T., Miranda, C., Mianga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission

Submitted (05-APR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

On Feb 26, 2001 this sequence version replaced gi:10800291.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www.seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L8880

Center clone name: 239_L-6

* NOTE: This record contains 55 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1 675: contig of 675 bp in length
776 775: gap of 100 bp
776 1454: contig of 679 bp in length
1455 1554: gap of 100 bp
1555 2252: contig of 698 bp in length
2253 2352: gap of 100 bp
2353 3021: contig of 669 bp in length
3022 3121: gap of 100 bp
3122 3804: contig of 683 bp in length
3805 3904: gap of 100 bp
3905 4583: contig of 679 bp in length
4584 4683: gap of 100 bp
4684 5365: contig of 682 bp in length
5366 5465: gap of 100 bp
5466 6156: contig of 691 bp in length
6157 6256: gap of 100 bp
6257 6951: contig of 695 bp in length
6952 7051: gap of 100 bp
7052 7734: contig of 683 bp in length
7735 7834: gap of 100 bp
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8517 8616: gap of 100 bp
8617 9303: contig of 687 bp in length
9304 9403: gap of 100 bp
9404 10080: contig of 677 bp in length
10081 10180: gap of 100 bp
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10867 10966: gap of 100 bp
10967 11666: contig of 700 bp in length
11667 11766: gap of 100 bp
11767 12454: contig of 688 bp in length
12455 12554: gap of 100 bp
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13247 13346: gap of 100 bp
13347 14025: contig of 679 bp in length
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15773 16463: contig of 691 bp in length
16464 16563: gap of 100 bp
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17235 17334: gap of 100 bp
17335 18038: contig of 704 bp in length
18039 18138: gap of 100 bp
18139 18836: contig of 698 bp in length
18837 18936: gap of 100 bp
18937 19636: contig of 700 bp in length
19637 19736: gap of 100 bp
19737 20416: contig of 680 bp in length
20417 20516: gap of 100 bp
20517 21224: contig of 708 bp in length
21225 21324: gap of 100 bp
21325 22003: contig of 679 bp in length
22004 22103: gap of 100 bp
22104 22792: contig of 689 bp in length
22793 22892: gap of 100 bp
22893 23580: contig of 688 bp in length
23581 23680: gap of 100 bp
23681 24384: contig of 704 bp in length
24385 24484: gap of 100 bp
24485 25199: contig of 715 bp in length
25200 25299: gap of 100 bp
25300 25956: contig of 657 bp in length
25957 26056: gap of 100 bp
26057 26726: contig of 670 bp in length
26727 26826: gap of 100 bp
26827 27504: contig of 678 bp in length
27505 27604: gap of 100 bp


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STIKWIDMLSDRRLDKSFLDMS"
6121. 6567
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gene_id:F16J14.4"
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SEHSLVINAIDQDSRCKFRMIGGLVLTKEVLPVQRNKGDLSEVVRKLYETLE
KKKDLTEPEAKYKIRITQEDNKEGKNKEGNAQGVLVGAASSQ"
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/codon_start=1
/evidence=not_experimental
/product="seed maturation protein, LEA protein in group
5-like"
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/db_xref="GI:11994281"
/translation="MSQEQPKRPQEPVYGVDFVSGELADKPIAPEDANMQAAET
RVFGHTQKGAAMQSAATANKRGFVHPGDTDLAARGVTVTAQDVPGARVITEF
VGVVYQGVPRVTAAMAEAVYGLSQAITIGALEATVYTAGNKPVDQSDAA
AIOAAEVACGTNVIAPGAGIAAQAASAAHNATIDREDKIKLIDVLGATGKLAADK
AVTORAEGVWSAELRNPNLSHTPGGVAASITAAARNERADI"
8334..8563
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unknown protein"
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/evidence=not_experimental
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RKIVYNLKSITIRIKQDDNKEGKNKEGNAQGVVKTILFSFGFLYCCICIGFF
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VFQHTQKGAAMQSAATNIRGGVHPDDKTELVAERGATVEOTVPAATVTFEFG
QGVVGVHPRVVAARTDEALQSTITIGALEATVYTAGNKPVDQSDAAAIQAAE
MRASGTNVIALGASQAADHATVDYDRDKIKLRDLVLTGAAGKLSADRAVTRED
AEGVSAEMRNPNKLTCTHPGVAASLTVAARNERVDI"
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strong similarity to unknown protein"
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/db_xref="GI:11994284"
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NUSDHLDTAQENDFWNGFSREAEIDPEPSQAKENGKRSVDNSATHGETDLNQL
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SFASKPOLARYLESDFPGMDADAFASFWSKVPALFQPAKPKYDAASLFEETPEVQTE
VGQNDNAQDGKRSRRTIOQGGAVDLNLFNEESEPAPAKTSPRSGSNKKKKGATTPAT
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VSSPMEYSAEARKNISLLEKDETTFLFSKDAAEIALATKLKBDNLTAEEIVRL
KLMEETPSEVFQENGVIEADRFPSALELNKAKVASLKEYESDLKEKKGLSIQNEV
DYNSETIRIDQIQALQARSELKRYIGTKEKERVDSYSGOKMVANSIPKVVQEVQS
ANLKPEWCECKKDNLAKREAEILSKFTPLKGFLL"
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gene_id:F16J14.9
similar to unknown protein"
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SLDELDVWRFRLPPESTRPELVTVACVDGLIVTPKNAEEDDDDDGGGDFQGGIGS
GRVLVQ"
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RSNTKLY"
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DTKPSYLKNPFGSDNPKTOEPETRLKLEKRIGLAIVDSLIODETPEPGPRSGTILF
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YTCVCHGPRTIHFDCNIVESQPVWFERSDPVNESDSISPPDPSFLSCCNCK
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RDMFLYSVRDDCFV"
complement(join(36967..37029,37472..37671,37881..38202))
Query Match 2.1%; Score 25; DB 8; Length 47827;
Best Local Similarity 100.0%; Pred. No. 0.096;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 35569 TTATTTCAAAAAAAAAAAAAAAAA 35545

RESULT 28
HSDJ753M9 57698 bp DNA 12-DEC-1999
LOCUS Human DNA sequence from clone RPA-753M9 on chromosome 22 Contains
DEFINITION EST and SPS, complete sequence.
ACCESSION AL079301
VERSION AL079301.14 GI:5725274
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 37698)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Direct Submission
JOURNAL Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
COMMENT On Aug 10, 1999 this sequence version replaced gi:5668660.
This sequence has been finished according to sequence map criteria

```

as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/chr22>

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP4-753M9 is from the library RPI-4 constructed at the Roswell Park Cancer

Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/>

VECTOR: pCYPAC2

IMPORTANT: This sequence is not the entire insert of clone

RP4-753M9. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone XX-PRY7CC1 is at 57599 in this sequence. The true right end of clone RPI-127B20 is at 100 in this sequence.

FEATURES

source Location/Qualifiers

1..57698
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="22"
 /clone_lib="RPI-4"
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 155..1810
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 1811..2136
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 2353..2656
 /note="AluSq repeat: matches 1..304 of consensus"
 4059..4283
 /note="MIR repeat: matches 12..262 of consensus"
 5327..5857
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 5658..6150
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 6151..6191
 /note="MIR repeat: matches 205..244 of consensus"
 8001..8160
 /note="HAL1 repeat: matches 811..959 of consensus"
 8196..8487
 /note="AluSp repeat: matches 8..299 of consensus"
 8794..8890
 /note="HAL1 repeat: matches 269..372 of consensus"
 8891..9232
 /note="AluY repeat: matches 1..306 of consensus"
 10366..10437
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 10844..11248
 /note="MLT2CB repeat: matches 1..430 of consensus"
 11249..11544
 /note="AluSq repeat: matches 3..298 of consensus"
 11545..11558
 /note="MLT2CB repeat: matches 430..442 of consensus"
 11562..11850
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 11851..12164

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 /note="L1P16 repeat: matches 5502..5858 of consensus"
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 12579..12920
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 12921..12972
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 14261..14498
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 17504..17812
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 17837..18620
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 18621..18653
 /note="MER46A repeat: matches 199..232 of consensus"
 18654..18956
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 18957..19169
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 19170..19308
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 19676..19984
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 20080..20211
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 20514..20561
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 21182..21268
 /note="MIR repeat: matches 103..199 of consensus"
 21293..21432
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 /note="L2 repeat: matches 2383..2511 of consensus"
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 26472..26759
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 27151..27431
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 27572..27870
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 28178..28549
 /note="L1ME repeat: matches 5536..5944 of consensus"
 28640..28950
 /note="AluSk repeat: matches 1..312 of consensus"
 29403..29464
 /note="L2 repeat: matches 2638..2701 of consensus"
 30073..30094
 /note="L1MB5 repeat: matches 6139..6160 of consensus"
 30095..30388
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 /note="L2 repeat: matches 2468..2705 of consensus"
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 /note="MIR repeat: matches 92..176 of consensus"
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 /note="MIR repeat: matches 109..174 of consensus"
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* 15520 16233: contig of 714 bp in length
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* 17144 17871: contig of 728 bp in length
* 17872 17971: gap of 100 bp
* 17972 18687: contig of 716 bp in length
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* 18788 19484: contig of 697 bp in length
* 19485 19584: gap of 100 bp
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* 20306 20405: gap of 100 bp
* 20406 21117: contig of 712 bp in length
* 21118 21217: gap of 100 bp
* 21218 21915: contig of 698 bp in length
* 21916 22015: gap of 100 bp
* 22016 22723: contig of 708 bp in length
* 22724 22823: gap of 100 bp
* 22824 23530: contig of 707 bp in length
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* 23631 24311: contig of 681 bp in length
* 24312 24411: gap of 100 bp
* 24412 25117: contig of 706 bp in length
* 25118 25217: gap of 100 bp
* 25218 25927: contig of 710 bp in length
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* 26028 26762: contig of 735 bp in length
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* 26863 27570: contig of 708 bp in length
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* 27671 28392: contig of 722 bp in length
* 28393 28492: gap of 100 bp
* 28493 29233: contig of 741 bp in length
* 29234 29333: gap of 100 bp
* 29334 30047: contig of 714 bp in length
* 30048 30147: gap of 100 bp
* 30148 30850: contig of 703 bp in length
* 30851 30950: gap of 100 bp
* 30951 31668: contig of 718 bp in length
* 31669 31768: gap of 100 bp
* 31769 32466: contig of 698 bp in length
* 32467 32566: gap of 100 bp
* 32567 33259: contig of 693 bp in length
* 33260 33359: gap of 100 bp
* 33360 34078: contig of 719 bp in length
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* 42914 43013: gap of 100 bp
* 43014 43744: contig of 731 bp in length
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* 48744 49458: contig of 715 bp in length
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* 50359 51103: contig of 745 bp in length
* 51104 51203: gap of 100 bp
* 51204 51922: contig of 719 bp in length
* 51923 52022: gap of 100 bp
* 52023 52729: contig of 707 bp in length
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* 53650 54357: contig of 708 bp in length
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* 54458 55160: contig of 703 bp in length
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Query Match          2.1%; Score 25; DB 2; Length 63331;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 30

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LOCUS Homo sapiens chromosome 15 clone RP11-507J18 map 15, LOW-PASS
DEFINITION SEQUENCE SAMPLING.
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ACCESSION AC090728
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VERSION AC090728.2 GI:13470213
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KEYWORDS HTG; HTGS_PHASE0.
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SOURCE human.
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ORGANISM

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE 1 (bases 1 to 73880)
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AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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TITLE Homo sapiens chromosome 15, clone RP11-507J18
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JOURNAL Unpublished
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REFERENCE 2 (bases 1 to 73880)
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AUTHORS Birren,B., Linton,L., Nusbaum,C.,
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Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (09-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 28, 2001 this sequence version replaced gi:13259447.

All repeats were identified using RepeatMasker:
Smith, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L12459
Center Clone name: 507_J_18

* NOTE: This record contains 84 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1 747: contig of 747 bp in length
* 748 847: gap of 100 bp
* 848 1634: contig of 787 bp in length
* 1635 1734: gap of 100 bp
* 1735 2518: contig of 784 bp in length
* 2519 2618: gap of 100 bp
* 2619 3406: contig of 788 bp in length
* 3407 3506: gap of 100 bp
* 3507 4276: contig of 770 bp in length
* 4277 4376: gap of 100 bp
* 4377 5167: contig of 791 bp in length
* 5168 5267: gap of 100 bp
* 5268 6047: contig of 780 bp in length
* 6048 6147: gap of 100 bp
* 6148 6919: contig of 772 bp in length
* 6920 7019: gap of 100 bp
* 7020 7837: contig of 818 bp in length
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* 9576 9675: gap of 100 bp
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* 13194 13974: contig of 781 bp in length
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* 16642 16741: gap of 100 bp
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20248 21034: contig of 787 bp in length
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21135 21911: contig of 777 bp in length
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23828 24612: contig of 785 bp in length
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41408 42184: contig of 777 bp in length
42185 42284: gap of 100 bp
42285 43066: contig of 782 bp in length
43067 43166: gap of 100 bp
43167 43945: contig of 779 bp in length
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45832 46631: contig of 800 bp in length
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* 57308 57407: gap of 100 bp
* 57408 58166: contig of 759 bp in length
* 58167 58266: gap of 100 bp
* 58267 59049: contig of 783 bp in length
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* 59150 59986: contig of 837 bp in length
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Query Match
Best Local Similarity 100.0%; Pred. No. 0.09; Length 73880;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1149 ttatttcaaaaaaaaaaaaaa 1173
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RESULT 31
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LOCUS
DEFINITION Homo sapiens chromosome 8 clone RP11-714P7 map 8, LOW-PASS SEQUENCE
ACCESSION AC034306
VERSION AC034306.2 GI:7549708
KEYWORDS HTG; HTGS_PHASE0.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 81447)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 8, clone RP11-714P7
Unpublished
2 (bases 1 to 81447)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Bada,F.,
Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
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O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
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Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo.A., Willson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (05-APR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

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COMMENT

On Apr 14, 2000 this sequence version replaced gi:7417884.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L9350
 Center clone name: 714_P_7

* NOTE: This record contains 96 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the record is updated, the accession number will
 * be preserved.

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 * 6699 7451: contig of 753 bp in length
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 * 19472 20154: contig of 683 bp in length
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 * 20255 21018: contig of 764 bp in length

Address for correspondence: kaos@kazusa.or.jp
 For the latest information on annotation of this clone, please see
<http://www.kazusa.or.jp/kaos/cgi-bin/agd-graph.cgi?c=MRG7>
 Genes with similarity to proteins in the databases are described in
 'product' or 'note' qualifiers. Genes that have no significant
 protein similarity are described as 'unknown protein'.
 The software programs used to predict genes include: Grail
 (Informatics Group, Oak Ridge National Laboratory,
<http://complib.oornl.gov/grail-1.3/>),
 GENSCAN (Chris Burge, MIT, <http://CBS-081.mit.edu/GENSCAN.html>),
 NetGene2 (S.M. Hebsgaard, et al., CCS, Technical University of
 Denmark, <http://www.cbs.dtu.dk/services/NetGene2/>) and
 SplicePredictor (Volker Brendel, Stanford University,
<http://gramlin1.zool.iastate.edu/cgi-bin/sp.cgi>).
 Genes encoding tRNAs are predicted by tRNAscan-SE
 (Sean Eddy, Washington University School of Medicine, St. Louis,
<http://genome.wustl.edu/eddy/tRNAscan-SE/>).
 This sequence may not be the entire insert of
 shorter because we remove overlaps between neighboring submissions.
 The 5' clone is MCM23

FEATURES
source

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 ILQHLGWSIEKNELYKDLPSROIKEVDPRTAVTTSSETEALRPMGIQDAINSEIK
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 /protein_id="BAB09468.1"
 /db_xref="GI:9758892"
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 PGFHGHHSFGDTNGICISGPHFNPLNRVHGPPEERHAGDNLNLAGSNGVAEI
 LIKXKHPLSGQSYILGRAVYVHADPDGLGGKHKLSKSGNAGSRVGGCIGIIGQSSA
 DAKL"
 complement(join(12611..12742,12828..12947,13106..13183,
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 gene_id:MRG7.7"
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 gene_id:MRG7.8"
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 /evidence=not_experimental
 /protein_id="BAB09470.1"
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 /translation="MNLWVSIFLVSAIAGSCILPSCGFAYVDVNCNHEFEVERSVIEQKCP
 RSLYFPPPEVDGDLDDLDMDANHGNAISILFYSCPPFRSRAVRPKFEDVLSSEPHI
 THLYVEQOALPVSFSGYIHSILPSILMWNQTMKMYHGPDKDLSLIQFYKETGESM
 LHEKPCVCLKPVQYMDGEPTSLDLDGNLITWLNHSGSSTRETAEREPMVLAJMF
 LSLKALILFIPMGSRKLTWALYVPHLSLGLTGETSQLFGRALHMIDVRRRLWLRL
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31569..31754)

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Best Local Similarity 100.0%; Pred. No. 0.088;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1149 ttattcaaaaaaaaaaaaaaaaa 1173
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Db 61644 TTATTCAAAAAAAAAAAAAAAAAA 61620

RESULT 33
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AC040952
VERSION    AC040952.1 GI:7534153
KEYWORDS   HTG; HTGS_PHASE0.
SOURCE     human.
ORGANISM   Homo sapiens
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REFERENCE  1 (bases 1 to 85812)
            Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
            Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
            Boguslavsky, L., Bouckgaltier, B., Brown, A., Burkett, G.,
            Campoliano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,
            Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S.,
            Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,
            Galdagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
            Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
            Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
            Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczek, J.,
            Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
            McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
            Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
            Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
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            Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
            Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
            Testaye, S., Theodore, J., Tirrell, A., Travers, M., Triggillo, J.,
            Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
            Young, G., Zainoun, J., Zimmer, A. and Zody, M.
Direct Submission
Submitted (11-APR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smith, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L9152
Center clone name: 2125_K_20
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* NOTE: This record contains 91 individual
* sequencing reads that have not been assembled into

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* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
* 1 828: contig of 828 bp in length
* 829 928: gap of 100 bp
* 929 1791: contig of 863 bp in length
* 1792 1891: gap of 100 bp
* 1892 2687: contig of 796 bp in length
* 2688 2787: gap of 100 bp
* 2788 3639: contig of 852 bp in length
* 3640 3739: gap of 100 bp
* 3740 4574: contig of 835 bp in length
* 4575 4674: gap of 100 bp
* 4675 5485: contig of 811 bp in length
* 5486 5585: gap of 100 bp
* 5586 6420: contig of 835 bp in length
* 6421 6520: gap of 100 bp
* 6521 7343: contig of 823 bp in length
* 7344 7443: gap of 100 bp
* 7444 8293: contig of 850 bp in length
* 8294 8393: gap of 100 bp
* 8394 9223: contig of 830 bp in length
* 9224 9323: gap of 100 bp
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* 10181 10280: gap of 100 bp
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* 12084 12183: gap of 100 bp
* 12184 13055: contig of 872 bp in length
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* 13156 14010: contig of 855 bp in length
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* 14111 14961: contig of 851 bp in length
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* 17904 18735: contig of 832 bp in length
* 18736 18835: gap of 100 bp
* 18836 19677: contig of 842 bp in length
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* 19778 20614: contig of 837 bp in length
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Query Match 2.1%; Score 25; DB 2; Length 85812;
 Best Local Similarity 100.0%; Pred. No. 0.088;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1149 ttatttcaaaaaaaaaaaaaa 1173
 Db 10593 TTATTTCAAAAAAAAAAAAAA 10569

RESULT 34

AC005646 86677 bp DNA HTG 10-DEC-1999
 Drosophila melanogaster chromosome 2 clone DS00968 (D404) map
 51B1-51B4 strain Y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 3
 unordered pieces.

AC005646
 AC005646.6 GI:6554236
 HTG; HTGS_PHASE1.
 fruit fly.

ORGANISM
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
 1 (bases 1 to 86677)
 Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G.,
 Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,
 Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L.,
 Hinkle, A., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K.,
 Kearney, L., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A.R.,
 Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B.,
 Richards, S., Sethi, H., Svirskas, R.R., Wan, K.H., Webster, D.,
 Woolley, P., Yang, S., Yee, M., Yu, C. and Rubin, G.M.
 Sequencing of Drosophila melanogaster
 Unpublished

2 (bases 1 to 86677)
 Celniker, S.E., George, R.A., Galle, R., Svirskas, R.R., Hoskins, R.A.,
 Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Chavez, C.,
 Chew, M., Doyle, C.M., Farfan, D.E., Flanagan, J., Houston, K.A.,
 Hummasti, S.R., Karra, K., Kearney, L., Kim, S.H., Lee, B.,
 Lomotan, M.A., Mak, J., Mazda, P., Mok, M.S., Moshrefi, A.R.,
 Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., PUNCH, E.,
 Snir, E., Twomey, B., Wan, K.H., Whitelaw, K.R., Yee, A., Zhang, R.,
 Zier, L.L. and Kimmel, B.E.
 Direct Submission
 Submitted (10-SEP-1998) Drosophila Genome Center, Lawrence Berkeley
 Laboratory, MS 64-121, Berkeley, CA 94720, USA
 On Dec 10, 1999 this sequence version replaced gi:5656719.
 For further information about this sequence, including its location
 and relationship to other sequences, please visit our sequence
 archive web site (<http://www.fruitfly.org/sequence/>) or send email
 to bdg@fruitfly.berkeley.edu. All contigs in this submission meet
 the following cutoffs: length >= 200 bases. P1 library location:
 8-11.

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 3 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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 * 297 376: gap of unknown length
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* Location/Qualifiers
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FEATURES
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VERSION	AL034556.3 GI:7711064	
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SOURCE	Serine/threonine protein	
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REFERENCE	Plasmodium falciparum	
AUTHORS	Eukaryota; Alveolata; Ap	
	1 (bases 1 to 86827)	
	Bowman, S., Lawson, D., Ba	
	Churcher, C.M., Craig, A.,	
	Gentles, S., Gwilliam, R.,	
	Hornsby, T., Horrocks, P.,	
	Moule, S., Mungall, K., Mu	
	Rajandream, M.-A., Rutter	
	Rajandream, J.E., Whitehead,	
	Barrell, B.G.	
TITLE	The complete nucleotide	
JOURNAL	falciparum	
MEDLINE	Nature 400 (6744), 532-5	
REFERENCE	99376085	
AUTHORS	2 (bases 1 to 86827)	
	Bowman, S., Skelton, J., C	
JOURNAL	Barrell, B.	
REFERENCE	Unpublished	
AUTHORS	3 (bases 1 to 86827)	
TITLE	Lawson, D., Bowman, S. and	
JOURNAL	Direct Submission	
	Submitted (17-DEC-1998)	
	The Sanger Centre, Welli	
	CB10 1SA, UK	
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 Db 34412 TTATTTCAAAAAAAAAAAAAA 34388

RESULT 36
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 VERSION AC010796.7 GI:12325034
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 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 1 (bases 1 to 87400)
 Wu,D., Maiti,R., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R.,
 Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
 Arabidopsis thaliana chromosome 1 BAC F24J13 genomic sequence
 Unpublished
 2 (bases 1 to 87400)
 Lin,X. and Kaul,S.
 Direct Submission
 Submitted (23-SEP-1999) The Institute for Genomic Research, 9712
 Medical Center Dr, Rockville, MD 20850, USA, xlinetigr.org
 3 (bases 1 to 87400)
 Town,C.D. and Kaul,S.
 Direct Submission
 Submitted (19-JAN-2001) The Institute for Genomic Research, 9712
 Medical Center Dr, Rockville, MD 20850, USA, cdtownetigr.org
 On Jan 19, 2001 this sequence version replaced gi:12280801.
 Address all correspondence to:at@tigr.org

BAC clone F24J13 is from Arabidopsis thaliana chromosome 1
 The orientation of the sequence is from SP6 to T7 end of the BAC
 clone.
 Genes were identified by a combination of several methods: Gene
 prediction programs including Genscan+ (Chris Burge,
 http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHM (Mark Borodovsky,
 http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant
 of GlimmerW, see Mihaela Pertea,
 http://www.tigr.org/softlab/glimmerm_hm/glimmerm.html, and
 GeneSplicer (Mihaela Pertea and Steven Salzberg, contact
 mpertea@tigr.org), searches of the complete sequence against a
 peptide database and the plant EST database at TIGR
 (http://www.tigr.org/tldb/tgi.shtml). Annotated genes are named to
 indicate the level of evidence for their annotation. Genes with
 similarity to other proteins are named after the database hits.
 Genes without significant peptide similarity but with EST
 similarity are named as unknown proteins. Genes without protein
 or EST similarity, that are predicted by more than two gene
 prediction programs over most of their length are annotated as
 hypothetical proteins. Genes encoding tRNAs are predicted by
 tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).
 Simple repeats are identified by repeatmasker (Arian Smit,
 http://ftp.genome.washington.edu/RM/RepeatMasker.html).

FEATURES
 Source
 1..87400
 /organism="Arabidopsis thaliana"
 /cultivar="Columbia"
 /db_xref="taxon:3702"
 /chromosome="1"
 /clone="F24J13"
 complement(<1..>433)

mRNA

Db 10154 TTATTTCAAAAAAAAAAAAAAAAAAAAA 10130

RESULT 37

AC007076

LOCUS

DEFINITION

AC007076 95477 bp DNA PRI 27-APR-2000
Homo sapiens PAC clone RP4-698F7 from 7p15.1-p13, complete
sequence.

AC007076

VERSION

AC007076.3

KEYWORDS

HTG.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

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JOURNAL

REFERENCE

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JOURNAL

Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/FTP/CHR7>, send mailto:egreen@nhgri.nih.gov, or see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

This clone was derived from human PAC library RPI-4, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor.

The clone may be obtained either from Genome Systems, Inc. (<http://www.genomesystems.com>) or Research Genetics, Inc. (<http://www.resgen.com>); or from Pieter de Jong.

VECTOR: pCYPAC2

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RP11-456N16, 200 bp overlap. Actual start of this clone is at base position 1 of RP4-698F7; actual end is at base position 16254 of RP11-456N16.

The sequence RP4-698F7 contains a tandem repeat from base position 38292 to 29389. The tandem size is believed to be in agreement with PCR and digest information. The tandem area falls within band sizes of 8391 insilico, 8452 real for ecorv; and 5096 insilico, 5128 real for hindiii.

FEATURES

Location/Qualifiers	Source
1..95477	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/chromosome="7"
	/map="7p15.1-p13"
	/clone="RP4-698F7"
	/clone_lib="RPI-4"
157..281	/rpt_family="MaLR"
730..901	/rpt_family="L2"
1596..1838	/rpt_family="MIR"
2317..2638	/rpt_family="Retroviral"
2863..3454	/rpt_family="Retroviral"
3500..3821	/rpt_family="Retroviral"
3950..4153	/rpt_family="Retroviral"
4154..4553	/rpt_family="Retroviral"
4557..5051	/rpt_family="L1"
5089..5119	/rpt_family="AT-rich"
5183..5439	/rpt_family="L1"
5450..5478	/rpt_family="L1"
5482..5723	/rpt_family="L1"
5744..6052	/rpt_family="Alu"
6307..6433	/rpt_family="L1"
6969..7546	/rpt_family="Retroviral"
9216..9463	/rpt_family="L1"
11308..11484	/db_xref="GI:1232262"
11392..11431	/rpt_family="(CA)n"

STS

repeat_region

AC007076 95477 bp DNA PRI 27-APR-2000
Homo sapiens PAC clone RP4-698F7 from 7p15.1-p13, complete
sequence.

AC007076
AC007076.3 GI:6604547
HTG.
human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 95477)
Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99063792

2 (bases 1 to 95477)
Ozersky, P., Kalicki, J. and Smith, R.
The sequence of Homo sapiens PAC clone RP4-698F7
Unpublished
3 (bases 1 to 95477)
Waterston, R.H.
Direct Submission
Submitted (13-MAR-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 95477)
Waterston, R.H.
Direct Submission
Submitted (19-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 95477)
Waterston, R.H.
Direct Submission
Submitted (21-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
6 (bases 1 to 95477)
Waterston, R.
Direct Submission
Submitted (27-APR-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Dec 20, 1999 this sequence version replaced gi:5001547.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc>
Contact: saplens@watson.wustl.edu
----- Summary Statistics

Center project name: H_DJ0698F07

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping

```

repeat_region 12041..12131
/rpt_family="MERL_type"
repeat_region 12186..12314
/rpt_family="MaLR"
/rpt_family="MaLR"
repeat_region 12315..12801
/rpt_family="MERL_type"
repeat_region 12802..13106
/rpt_family="MaLR"
repeat_region 13918..13968
/rpt_family="L1"
repeat_region 13971..13997
/rpt_family="TTTC)n"
repeat_region 13998..14285
/rpt_family="Alu"
repeat_region 14286..14685
/rpt_family="L1"
repeat_region 17206..17506
/rpt_family="Alu"
repeat_region 18905..19246
/rpt_family="L1"
repeat_region 20906..21274
/rpt_family="MaLR"
repeat_region 21432..21452
/rpt_family="AT-rich"
repeat_region 24864..24892
/rpt_family="(T)n"
misc_feature 24888..25144
/notes="similar to EST AW085212 (NID:g6040364) xe07c06.x1"
repeat_region 25373..26235
/rpt_family="L1"
repeat_region 26225..26700
/rpt_family="L1"
repeat_region 26732..26844
/rpt_family="Alu"
repeat_region 27061..27096
/rpt_family="AT-rich"
repeat_region 27262..27311
/rpt_family="Alu"
repeat_region 27313..27470
/rpt_family="(GAAA)n"
repeat_region 27530..27699
/rpt_family="Retroviral"
repeat_region 27902..27992
/rpt_family="MERL_type"
repeat_region 27991..28081
/rpt_family="MERL_type"
repeat_region 28097..28225
/rpt_family="L1"
repeat_region 28284..28442
/rpt_family="MERL_type"
repeat_region 28311..28464
/rpt_family="MERL_type"
STS complement(29279..29700)
/db_xref="GI:5223519"
repeat_region 29862..29963
/rpt_family="MIR"
repeat_region 31105..31222
/rpt_family="L1"
repeat_region 31242..31553

```

Query Match 2.1%; Score 25; DB 9; Length 95477;
 Best Local Similarity 100.0%; Pred. No. 0.086;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaa 1173
 |||||

DB 17482 TTATTTCACAAAAA 17506

RESULT 38
 AL356791 101157 bp DNA PRI 12-JAN-2001
 LOCUS Human DNA sequence from clone RP11-8013 on chromosome 9 Contains
 DEFINITION

GSSs and STSs, complete sequence.

AL356791

AL356791.9 GI:11877989

HTG.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 101157)

Barker, D.

Direct Submission

Submitted (05-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,

CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk

requests: clonerequest@sanger.ac.uk

On Dec 17, 2000 this sequence version replaced gi:11863404.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

This sequence has been finished according to sequence map criteria

as follows. An attempt is made to resolve all sequencing problems,

such as compressions and repeats, but not necessarily within known

annotated repeat sequence elements. Where the sequence is

ambiguous, there is an annotation using the 'unsure' feature key.

The following abbreviations are used to associate primary accession

numbers given in the feature table with their source databases:

Em; EMBL; Sw; SWISSPROT; Tr; TREMBL; Wp; WORMPEP; Information

on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence

was generated from part of bacterial clone contigs of human

chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping

Group. Further information can be found at

http://www.sanger.ac.uk/HGP/Chr9

RP11-8013 is from the library RP11-11.1 constructed by the group of

Pieter de Jong. For further details see

http://www.chori.org/bacpac/home.htm

VECTOR: pBACE3.6

IMPORTANT: This sequence is not the entire insert of clone

RP11-8013 It may be shorter because we sequence overlapping

sections only once, except for a 100 base overlap.

The true right end of clone RP11-8013 is at 101157 in this

sequence. The true right end of clone RP11-47769 is at 100 in this

sequence.

FEATURES

Source

Location/Qualifiers

1..101157

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="9"

/clone="RP11-8013"

/clone_lib="RPC1-11.1"

256..393

/note="L2 repeat: matches 2602..2746 of consensus"

complement(581..1430)

/note="match: STS: Em:G62385"

complement(791..1461)

/note="match: GSS: Em:AQ480671"

complement(921..1451)

/note="match: GSS: Em:AQ570464"

complement(1069..1461)

/note="match: GSS: Em:AQ664824"

complement(1098..1382)

/note="match: GSS: Em:AQ594692"

1134..1177

/note="MIR repeat: matches 97..139 of consensus"

complement(1967..2460)

/note="match: GSS: Em:AQ412192"

2191..2450

/note="AluX repeat: matches 1..260 of consensus"

complement(2692..3207)

/note="match: GSS: Em:A2519746"

2873..2886

repeat_region

```
repeat_region /note="L1MA7 repeat: matches 6154. .6166 of consensus"
3071. .3759
repeat_region /note="L2 repeat: matches 1984. .2750 of consensus"
4348. .4732
repeat_region /note="MLT2A repeat: matches 8. .397 of consensus"
4735. .4758
repeat_region /note="6 copies 4 mer ctct 100% conserved"
4763. .4862
repeat_region /note="HERVL repeat: matches 139. .238 of consensus"
4863. .5630
repeat_region /note="192 copies 4 mer atat 66% conserved"
5630. .5775
repeat_region /note="73 copies 2 mer at 80% conserved"
5631. .5822
repeat_region /note="48 copies 4 mer tata 73% conserved"
5823. .5861
repeat_region /note="MLT2A repeat: matches 407. .449 of consensus"
5862. .11474
repeat_region /note="HERVL repeat: matches 1. .5654 of consensus"
11475. .11780
repeat_region /note="MLT2B repeat: matches 1. .313 of consensus"
11797. .11834
repeat_region /note="MLT2A repeat: matches 416. .453 of consensus"
11876. .11929
repeat_region /note="MLT1F repeat: matches 76. .127 of consensus"
12146. .12201
repeat_region /note="L2 repeat: matches 2650. .2705 of consensus"
14674. .14741
misc_feature /note="34 copies 2 mer aa 73% conserved"
16776. .17286
repeat_region /note="match: GSS: Em:AQ150535"
16939. .17230
repeat_region /note="L1PA9 repeat: matches 5853. .6161 of consensus"
17319. .17439
repeat_region /note="FRAM_C repeat: matches 1. .121 of consensus"
18321. .18476
misc_feature /note="MIR repeat: matches 47. .204 of consensus"
18480. .18673
misc_feature /note="match: GSS: Em:AQ070516"
complement(19222. .19612)
repeat_region /note="match: GSS: Em:AQ535364"
20239. .20284
repeat_region /note="L2 repeat: matches 2460. .2486 of consensus"
20265. .20565
repeat_region /note="AluY repeat: matches 1. .302 of consensus"
20566. .20767
repeat_region /note="L2 repeat: matches 2486. .2673 of consensus"
20770. .20841
repeat_region /note="L2 repeat: matches 2670. .2743 of consensus"
21026. .22427
repeat_region /note="L2 repeat: matches 857. .2417 of consensus"
22439. .22500
repeat_region /note="L2 repeat: matches 2687. .2750 of consensus"
22894. .23016
misc_feature /note="3 copies 41 mer 77% conserved"
23116. .23798
misc_feature /note="match: GSS: Em:B82580"
23165. .23625
misc_feature /note="match: GSS: Em:AQ896235"
complement(23562. .24064)
misc_feature /note="match: GSS: Em:AQ555111"
complement(23656. .24064)
misc_feature /note="match: GSS: Em:AQ299045"
complement(24055. .24524)
repeat_region /note="match: GSS: Em:AQ720866"
24096. .24405
repeat_region /note="AluY repeat: matches 3. .302 of consensus"
24948. .25184
repeat_region /note="MIR repeat: matches 10. .262 of consensus"
25350. .25501
repeat_region /note="FRAM repeat: matches 1. .156 of consensus"
26263. .26296
repeat_region /note="17 copies 2 mer aa 88% conserved"
```

```
repeat_region 26384. .26466
/note="MIR repeat: matches 28. .111 of consensus"
26811. .27106
repeat_region /note="AluX repeat: matches 1. .296 of consensus"
28376. .28568
repeat_region /note="MLT1I repeat: matches 211. .403 of consensus"
31895. .32057
repeat_region /note="MERSB repeat: matches 1. .174 of consensus"
32239. .32366
repeat_region /note="MER7A repeat: matches 1. .126 of consensus"
32378. .32614
repeat_region /note="MER33 repeat: matches 52. .296 of consensus"
32977. .33137
repeat_region /note="MIR repeat: matches 2. .163 of consensus"
33249. .33488
repeat_region /note="L2 repeat: matches 2434. .2710 of consensus"
34725. .35062
repeat_region /note="MER7A repeat: matches 1. .346 of consensus"
35513. .35598
repeat_region /note="MIR repeat: matches 117. .197 of consensus"
35788. .35956
repeat_region /note="MIR repeat: matches 37. .215 of consensus"
37248. .37374
misc_feature /note="L2 repeat: matches 2574. .2688 of consensus"
complement(37683. .38110)
repeat_region /note="match: GSS: Em:AQ764674"
38347. .38630
repeat_region /note="AluY repeat: matches 1. .298 of consensus"
40121. .40238
repeat_region /note="MLT1J repeat: matches 1. .120 of consensus"
40884. .41367
repeat_region /note="MLT2CB repeat: matches 1. .501 of consensus"
43159. .43364
repeat_region /note="L2 repeat: matches 2307. .2507 of consensus"
43438. .43655
repeat_region /note="MER20 repeat: matches 1. .218 of consensus"
44967. .45042
repeat_region /note="L2 repeat: matches 2607. .2691 of consensus"
45072. .45380
misc_feature /note="AluSq repeat: matches 1. .308 of consensus"
45200. .45641
misc_feature /note="match: GSS: Em:AQ461292"
complement(46363. .46835)
repeat_region /note="match: GSS: Em:AQ407114"
46653. .46992
misc_feature /note="MER6IA repeat: matches 4. .354 of consensus"
46837. .47247
repeat_region /note="match: GSS: Em:AQ459068"
48337. .48645
repeat_region /note="AluJo repeat: matches 2. .310 of consensus"
51443. .51565
repeat_region /note="L2 repeat: matches 2103. .2228 of consensus"
```

Query Match 2.1%; Score 25; DB 9; Length 101157;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
|||||
DB 83293 TTATTTCACAAAAAAAAAAAAAAAAA 83317

RESULT 39
AC008623/c

LOCUS AC008623 128266 bp DNA PRI 07-NOV-2000
DEFINITION Homo sapiens chromosome 19 clone CTP-14D10, complete sequence.
ACCESSION AC008623
VERSION AC008623.4 GI:11119446
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.


```

* 6946 7045: gap of 100 bp
* 7046 7929: contig of 884 bp in length
* 7930 8029: gap of 100 bp
* 8030 8945: contig of 916 bp in length
* 8946 9045: gap of 100 bp
* 9046 9947: contig of 902 bp in length
* 9948 10047: gap of 100 bp
* 10048 10962: contig of 915 bp in length
* 10963 11062: gap of 100 bp
* 11063 11963: contig of 901 bp in length
* 11964 12063: gap of 100 bp
* 12064 12974: contig of 911 bp in length
* 12975 13074: gap of 100 bp
* 13075 13990: contig of 916 bp in length
* 13991 14090: gap of 100 bp
* 14091 14956: contig of 866 bp in length
* 14957 15056: gap of 100 bp
* 15057 15925: contig of 869 bp in length
* 15926 16025: gap of 100 bp
* 16026 16936: contig of 911 bp in length
* 16937 17036: gap of 100 bp
* 17037 17958: contig of 922 bp in length
* 17959 18058: gap of 100 bp
* 18059 18959: contig of 901 bp in length
* 18960 19059: gap of 100 bp
* 19060 19957: contig of 898 bp in length
* 19958 20057: gap of 100 bp
* 20058 20951: contig of 894 bp in length
* 20952 21051: gap of 100 bp
* 21052 21931: contig of 880 bp in length
* 21932 22031: gap of 100 bp
* 22032 22921: contig of 890 bp in length
* 22922 23021: gap of 100 bp
* 23022 23906: contig of 885 bp in length
* 23907 24006: gap of 100 bp
* 24007 24889: contig of 883 bp in length
* 24890 24989: gap of 100 bp
* 24990 25882: contig of 893 bp in length
* 25883 25982: gap of 100 bp
* 25983 26881: contig of 899 bp in length
* 26882 26981: gap of 100 bp
* 26982 27892: contig of 911 bp in length
* 27893 27992: gap of 100 bp
* 27993 28908: contig of 916 bp in length
* 28909 29008: gap of 100 bp
* 29009 29860: contig of 852 bp in length
* 29861 29960: gap of 100 bp
* 29961 30853: contig of 893 bp in length
* 30854 30953: gap of 100 bp
* 30954 31868: contig of 915 bp in length
* 31869 31968: gap of 100 bp
* 31969 32859: contig of 891 bp in length
* 32860 32959: gap of 100 bp
* 32960 33849: contig of 890 bp in length
* 33850 33949: gap of 100 bp
* 33950 34823: contig of 874 bp in length
* 34824 34923: gap of 100 bp
* 34924 35803: contig of 880 bp in length
* 35804 35903: gap of 100 bp
* 35904 36787: contig of 884 bp in length
* 36788 36887: gap of 100 bp
* 36888 37761: contig of 874 bp in length
* 37762 37861: gap of 100 bp
* 37862 38769: contig of 908 bp in length
* 38770 38869: gap of 100 bp
* 38870 39774: contig of 905 bp in length
* 39775 39874: gap of 100 bp
* 39875 40761: contig of 887 bp in length
* 40762 40861: gap of 100 bp
* 40862 41777: contig of 916 bp in length
* 41778 41877: gap of 100 bp
* 41878 42788: contig of 911 bp in length
* 42789 42888: gap of 100 bp

```

```

* 42889 43774: contig of 886 bp in length
* 43775 43874: gap of 100 bp
* 43875 44776: contig of 902 bp in length
* 44777 44876: gap of 100 bp
* 44877 45738: contig of 862 bp in length
* 45739 45838: gap of 100 bp
* 45839 46717: contig of 879 bp in length
* 46718 46817: gap of 100 bp
* 46818 47723: contig of 906 bp in length
* 47724 47823: gap of 100 bp
* 47824 48717: contig of 894 bp in length
* 48718 48817: gap of 100 bp
* 48818 49736: contig of 919 bp in length
* 49737 49836: gap of 100 bp
* 49837 50744: contig of 908 bp in length
* 50745 50844: gap of 100 bp
* 50845 51751: contig of 907 bp in length
* 51752 51851: gap of 100 bp
* 51852 52738: contig of 887 bp in length
* 52739 52838: gap of 100 bp
* 52839 53752: contig of 914 bp in length
* 53753 53852: gap of 100 bp
* 53853 54749: contig of 897 bp in length
* 54750 54849: gap of 100 bp
* 54850 55747: contig of 898 bp in length
* 55748 55847: gap of 100 bp
* 55848 56755: contig of 908 bp in length
* 56756 56855: gap of 100 bp
* 56856 57738: contig of 883 bp in length
* 57739 57838: gap of 100 bp
* 57839 58743: contig of 905 bp in length
* 58744 58843: gap of 100 bp
* 58844 59758: contig of 915 bp in length
* 59759 59858: gap of 100 bp
* 59859 60758: contig of 900 bp in length
* 60759 60858: gap of 100 bp
* 60859 61748: contig of 890 bp in length
* 61749 61848: gap of 100 bp
* 61849 62731: contig of 883 bp in length
* 62732 62831: gap of 100 bp
* 62832 63750: contig of 919 bp in length
* 63751 63850: gap of 100 bp
* 63851 64725: contig of 875 bp in length
* 64726 64825: gap of 100 bp
* 64826 65738: contig of 913 bp in length
* 65739 65838: gap of 100 bp
* 65839 66734: contig of 896 bp in length
* 66735 66834: gap of 100 bp
* 66835 67729: contig of 895 bp in length
* 67730 67829: gap of 100 bp
* 67830 68709: contig of 880 bp in length
* 68710 68809: gap of 100 bp
* 68810 69695: contig of 886 bp in length
* 69696 69795: gap of 100 bp
* 69796 70681: contig of 886 bp in length
* 70682 70781: gap of 100 bp
* 70782 71663: contig of 882 bp in length
* 71664 71763: gap of 100 bp
* 71764 72649: contig of 886 bp in length

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Query Match 2.1%; Score 25; DB 2; Length 144075;
 Best Local Similarity 100.0%; Pred. No. 0.081;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1149 ttattcaaaaaaaaaaaaaaa 1173
 |||||
 Db 113280 TTATTCAAAAAAAAAAAAAA 113304

RESULT 44
 AC023459/C
 LOCUS
 DEFINITION Homo sapiens chromosome 20 clone RP11-778f12 map 20, WORKING DRAFT

HTG
 09-MAR-2000


```

SEQUENCE, 35 unordered pieces.
AC023459
AC023459.2 GI:7212060
HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE
human
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 146574)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 20, clone RP11-778F12
Unpublished
2 (bases 1 to 146574)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bedalov,F., Boguslavsky,L.,
Bouckhaghter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
Choehel,Y., Collangelo,M., Collins,S., Collymore,A., Cooke,P.,
DeArelano,K., Dewar,K., Dodge,S., Domino,M., Doyle,M.,
Fenster,J., Ferreira,P., FitzHugh,W., Forrest,C., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., Landers,T., Largocque,K., Lehoczy,J., Levine,R.,
Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M.,
McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Melidrim,J.,
Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Olivari,T.M.,
Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C.,
Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A.,
Travers,M., Trifilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B.,
Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and
Zody,M.
Direct Submission
Submitted (14-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 9, 2000 this sequence version replaced gi:6970679.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L6806
Center clone name: 778_F12
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 125661 bases at least Q40
Consensus quality: 136002 bases at least Q30
Consensus quality: 140407 bases at least Q20
Insert size: 153000; agarose-fp
Quality coverage: 3.1 in Q20 bases; agarose-fp
Quality coverage: 3.3 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 35 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 1237: contig of 1237 bp in length
* 1238 1337: gap of 100 bp
* 1338 2544: contig of 1207 bp in length
* 2545 2644: gap of 100 bp
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FEATURES
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/db_xref="taxon:9606"
/chromosome="20"
/map="20"
/clone="RP11-778F12"
/clone_lib="RPC1-11 Human Male BAC"

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3876 3975: gap of 100 bp
3976 4979: contig of 1004 bp in length
4980 5079: gap of 100 bp
5080 6340: contig of 1261 bp in length
6341 6440: gap of 100 bp
6441 7861: contig of 1421 bp in length
7862 7961: gap of 100 bp
7962 10255: contig of 2294 bp in length
10256 10355: gap of 100 bp
10356 11708: contig of 1353 bp in length
11709 11808: gap of 100 bp
11809 13578: contig of 1770 bp in length
13579 13678: gap of 100 bp
13679 15557: contig of 1879 bp in length
15558 15657: gap of 100 bp
15658 18218: contig of 2561 bp in length
18219 18318: gap of 100 bp
18319 20366: contig of 2048 bp in length
20367 20466: gap of 100 bp
20467 22083: contig of 1617 bp in length
22084 22183: gap of 100 bp
22184 24286: contig of 2103 bp in length
24287 24386: gap of 100 bp
24387 26707: contig of 2321 bp in length
26708 26807: gap of 100 bp
26808 28595: contig of 1788 bp in length
28596 28695: gap of 100 bp
28696 32080: contig of 3385 bp in length
32081 32180: gap of 100 bp
32181 35723: contig of 3543 bp in length
35724 35823: gap of 100 bp
35824 39694: contig of 3871 bp in length
39695 39794: gap of 100 bp
39795 42580: contig of 2786 bp in length
42581 42680: gap of 100 bp
42681 45710: contig of 3030 bp in length
45711 45810: gap of 100 bp
45811 51060: contig of 5250 bp in length
51061 51160: gap of 100 bp
51161 54715: contig of 3555 bp in length
54716 54815: gap of 100 bp
54816 59462: contig of 4647 bp in length
59463 59562: gap of 100 bp
59563 65496: contig of 5934 bp in length
65497 65596: gap of 100 bp
65597 70515: contig of 4919 bp in length
70516 70615: gap of 100 bp
70616 75951: contig of 5336 bp in length
75952 76051: gap of 100 bp
76052 81156: contig of 5105 bp in length
81157 81256: gap of 100 bp
81257 88039: contig of 6783 bp in length
88040 88139: gap of 100 bp
88140 94185: contig of 6046 bp in length
94186 94285: gap of 100 bp
94286 103388: contig of 9103 bp in length
103389 103488: gap of 100 bp
103489 114282: contig of 10794 bp in length
114283 114382: gap of 100 bp
114383 124249: contig of 9867 bp in length
124250 124349: gap of 100 bp
124350 134963: contig of 10614 bp in length
134964 135063: gap of 100 bp
135064 146574: contig of 11511 bp in length.

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Fri Dec 28 09:12:30 2001

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misc_feature 3976. 4979
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misc_feature 5080. 6340
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misc_feature 28696. 32080
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/note="assembly_fragment"
misc_feature 45811. 51060
/note="assembly_fragment"
misc_feature 51161. 54715
/note="assembly_fragment"
misc_feature 54816. 59462
/note="assembly_fragment"
misc_feature 59563. 65496
/note="assembly_fragment"

Query Match 2.1%; Score 25; DB 2; Length 146574;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1149 ttatttcaaaaaaaaaaaaaa 1173
Db 5827 TTATTTCAAAAAAAAAAAAAA 5803

RESULT 45
AC023196/c DNA HTG 01-MAR-2000
LOCUS AC023196 147246 bp
DEFINITION Homo sapiens clone RP11-395C3, WORKING DRAFT SEQUENCE, 26 unordered
pieces.
ACCESSION AC023196
VERSION AC023196.2 GI:7139743
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 147246)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-395C3
Unpublished
2 (bases 1 to 147246)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Bada,F.,
Boguslavsky,L., Bouknight,B., Brown,A., Burkett,G., Castle,A.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
DeArellano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J.,
Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
McPheeters,R., Meldrum,J., Meneus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Olivari,T.M., Peterson,K.,
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (09-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 1, 2000 this sequence version replaced gi:6957785.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: W18R
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L5884
Center clone name: 395_C_3
----- Summary Statistics
Sequencing vector: M13: M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 135851 bases at least Q40
Consensus quality: 141251 bases at least Q30
Consensus quality: 143252 bases at least Q20
Insert size: 155000; agarose-fp
Insert size: 144746; sum-of-contigs
Quality coverage: 4.3 in Q20 bases; agarose-fp
Quality coverage: 4.6 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 26 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved. 1212: contig of 1212 bp in length
1
1213 1312: gap of 100 bp
1313 2624: contig of 1312 bp in length
2625 2724: gap of 100 bp
2725 4183: contig of 1459 bp in length
4184 4283: gap of 100 bp
4284 5963: contig of 1680 bp in length
5964 6063: gap of 100 bp
6064 7954: contig of 1891 bp in length
7955 8054: gap of 100 bp
8055 9299: contig of 1245 bp in length
9300 9399: gap of 100 bp
9400 11758: contig of 2359 bp in length
11759 11858: gap of 100 bp
11859 14613: contig of 2755 bp in length

```

REFERENCE

AUTHORS

Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
 Barna,N., Bastien,V., Boguslavsky,L., Bouckgalter,B., Brown,A.,
 Camarata,J., Campopiano,A., Chang,J., Choepel,Y., Colangelo,M.,
 Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K.,
 Diaz,J.S., Dodge,S., Fero,S., Ferreira,P., FitzHugh,W., Gage,D.,
 Galagan,J., Gardyna,S., Glnde,S., Goyette,M., Graham,L.,
 Grand-Pierre,N., Hegos,B., Hearford,A., Horton,L., Hulme,W.,
 Iliev,I., Johnson,R., Jones,C., Karatas,A., LaRocque,K.,
 Lamazares,C., Macdonald,P., Lehocsky,J., Levine,R., Liu,G.,
 MacLean,K., Landers,T., Lehocsky,J., Matthews,C., McCarthy,M.,
 McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L.,
 Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
 Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
 Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
 Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R., Seaman,S.,
 Severy,P., Sougnuez,C., Spencer,B., Stange-Thomann,N.,
 Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,
 Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE

JOURNAL

COMMENT

Submitted (31-MAY-2001) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On May 31, 2001 this sequence version replaced g1:14150912.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WtBR

Web site: <http://www-seq.wi.mit.edu>Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L1085

Center clone name: 44_K_6

FEATURES

source	Location/Qualifiers
repeat_region	1. 149008
repeat_region	/organism="Homo sapiens"
repeat_region	/db_xref="taxon:9606"
repeat_region	/clone="RP11-44K6"
repeat_region	/clone_lib="RPC1-11 Human Male BAC"
repeat_region	649..785
repeat_region	/rpt_family="L1M4"
repeat_region	complement(793..963)
repeat_region	/rpt_family="AluSx"
repeat_region	complement(1261..1611)
repeat_region	/rpt_family="MLT1A2"
repeat_region	complement(1744..2041)
repeat_region	/rpt_family="AluY"
repeat_region	1766..1768
repeat_region	/note="possibly GGA or GAA"
repeat_region	2221..2326
repeat_region	/rpt_family="AluSx"
repeat_region	2327..2637
repeat_region	/rpt_family="AluSp"
repeat_region	2638..2817
repeat_region	/rpt_family="AluSx"
repeat_region	3614..3915
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repeat_region	4053..4212
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repeat_region	complement(4949..5384)
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repeat_region	complement(7892..8229)
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repeat_region	8254..8329
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repeat_region	/rpt_family="L1MEC"	Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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repeat_region	31462..31605		
repeat_region	/rpt_family="AluJo/FLAM"		
repeat_region	31608..31948		
repeat_region	/rpt_family="AluSx"		
repeat_region	33832..33856		
repeat_region	/rpt_family="AT-rich"		
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Best Local Similarity	100.0%; Pred. No. 0.08;		
Matches	25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY 1149	ttatttcaaaaaaaaaaaaaa 1173		
DB 29627	TTATTTCAAAAAAAAAAAAA 29603		
RESULT 47			
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LOCUS	PFMALP1 152409 bp DNA HTG 11-AUG-1999		
DEFINITION	Plasmodium falciparum chromosome 1 strain 3D7, *** SEQUENCING IN		
ACCESSION	AL031744		
VERSION	AL031744.7 GI:5731887		
KEYWORDS	HTG; HTGS_PHASE1.		
SOURCE	malaria parasite P. falciparum.		
ORGANISM	Plasmodium falciparum		
REFERENCE	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.		
AUTHORS	1 (bases 1 to 152409)		
TITLE	Bowman,S., Churcher,C., Harris,B., Harris,D., Lawson,D., Quail,M.		
JOURNAL	and Barrell,B.		
COMMENT	Submitted (24-SEP-1998) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK		
	On Aug 12, 1999 this sequence version replaced gi:5706481.		
	For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P.falciparum. IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc.		
	Order of segments is not known; 800 n's separate segments.		
	* NOTE: This is a 'working draft' sequence.		
	* This record will be updated with the finished sequence		
	* as soon as it is available and the accession number will		
	* be preserved.		
FEATURES	Location/Qualifiers		
source	1..152409		
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	/strain="3D7"		
	/db_xref="taxon:5833"		
	/chromosome="1"		
BASE COUNT	52517 a 14209 c 13674 g 51206 t 20803 others		
ORIGIN			


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RESULT 49
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AC AC073662;
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SV AC073662.2
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XX 06-JUL-2000 (Rel. 64, Created)
DT 24-JUL-2000 (Rel. 64, Last updated, Version 2)
XX
DE Homo sapiens chromosome 4 clone RP11-59815 map 4, WORKING DRAFT SEQUENCE,
DE 23 unordered pieces.
XX
XX HTG; HTGS_DRAFT; HTGS_PHASE1.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
XX [1]
XX 1-156847
XX Birren B., Linton L., Nusbaum C., Lander E.,
XX "Homo sapiens chromosome 4, clone RP11-59815";
XX Unpublished.
XX
XX [2]
XX 1-156847
XX Birren B., Linton L., Nusbaum C., Lander E., Abraham H., Allen N.,
XX Anderson S., Baldwin J., Barna N., Bastien V., Bida F., Boguslavsky L.,
XX Boukhalter B., Brown A., Burkett G., Campopiano A., Castle A., Choepel Y.,
XX Colangelo M., Collins S., Collymore A., Cooke P., DeArrellano K., Dewar K.,
XX Diaz J.S., Dodge S., Domino M., Doyle M., Ferreira P., FitzHugh W.,
XX Gage D., Galagan J., Gardyna S., Ginde S., Goyette M., Graham L.,
XX Grand-Pierre N., Grant G., Hagos B., Heaford A., Horton L., Howland J.C.,
XX Iliev I., Johnson R., Jones C., Kann L., Karatas A., Klein J., Lacroque K.,
XX Lamazares R., Landers T., Lehoczyk J., Levine R., Lieu C., Liu G.,
XX Locke K., Macdonald P., Marquis N., McCarthy M., McEwan P., McGurk A.,
XX McKernan K., McPheeters R., Meldrum J., Meneus L., Mihova T., Miranda C.,
XX Mienga V., Morrow J., Murphy T., Naylor J., Norman C.H., O'Connor T.,
XX O'Donnell P., O'Neill D., Ollivar T.M., Oliver J., Peterson K., Pierre N.,
XX Pisani C., Pollara V., Raymond C., Riley R., Rogov P., Rothman D., Roy A.,
XX Santos R., Schauer S., Severy P., Spencer B., Stange-Thomann N.,
XX Stojanovic N., Subramanian A., Talamas J., Tesfaye S., Theodore J.,
XX Tirrell A., Travers M., Trigilio J., Vassiliev H., Viel R., Vo A.,
XX Wilson B., Wu X., Wyman D., Ye W.J., Young G., Zainoun J., Zimmer A.,
XX Zody M.;
XX
XX Submitted (28-JUN-2000) to the EMBL/GenBank/DBJ databases.
XX Whitehead Institute/MIT Center for Genome Research, 320 Charles Street,
XX Cambridge, MA 02141, USA
XX
XX On Jul 22, 2000 this sequence version replaced gi:8783350.
XX All repeats were identified using RepeatMasker:
XX Smit, A.F.A. & Green, P. (1996-1997)
XX http://ftp.genome.washington.edu/RM/RepeatMasker.html
XX
XX ----- Genome Center
XX
XX Center: Whitehead Institute/ MIT Center for Genome Research
XX
XX Center code: WIBR
XX Web site: http://www-seq.wi.mit.edu
XX Contact: sequence_submissions@genome.wi.mit.edu
XX ----- Project Information
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XX Center project name: I9561
XX
XX Center clone name: 598_I_5
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XX ----- Summary Statistics
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XX Sequencing vector: M13; M77815; 100% of reads
XX Chemistry: Dye-terminator Big Dye; 100% of reads
XX Assembly program: Phrap; version 0.960731
XX Consensus quality: 144955 bases at least Q40
XX Consensus quality: 150878 bases at least Q30
XX Consensus quality: 153325 bases at least Q20
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Insert size: 156447; sum-of-contigs
Quality coverage: 4.0 in Q20 bases; agarose-fp
Quality coverage: 4.0 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 23 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 70065 80575: contig of 10511 bp in length
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* 105535 105634: gap of 100 bp
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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SEQUENCE, 2 ordered pieces.
ACCESSION AC083838
VERSION AC083838.3 GI:13357299
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 157525)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 8, clone RP11-42L4
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 157525)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bada,F., Boguslavskiy,L.,

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TITLE JOURNAL

COMMENT

Submitted (03-OCT-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 16, 2001 this sequence version replaced gi:12229345.
All repeats were identified using RepeatMasker.
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

Project Information
Center project name: L11292
Center clone name: 42_L4

Summary Statistics
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 156921 bases at least Q40
Consensus quality: 157145 bases at least Q30
Consensus quality: 157310 bases at least Q20
Insert size: 157000; agarose-fp
Insert size: 157425; sum-of-contigs
Quality coverage: 14.1 in Q20 bases; agarose-fp
Quality coverage: 14.1 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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* 77203 77302: gap of 100 bp
* 77303 157525: contig of 80223 bp in length.
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/chromosome="8"
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misc_feature

us-09-435-054-1.0110.rge

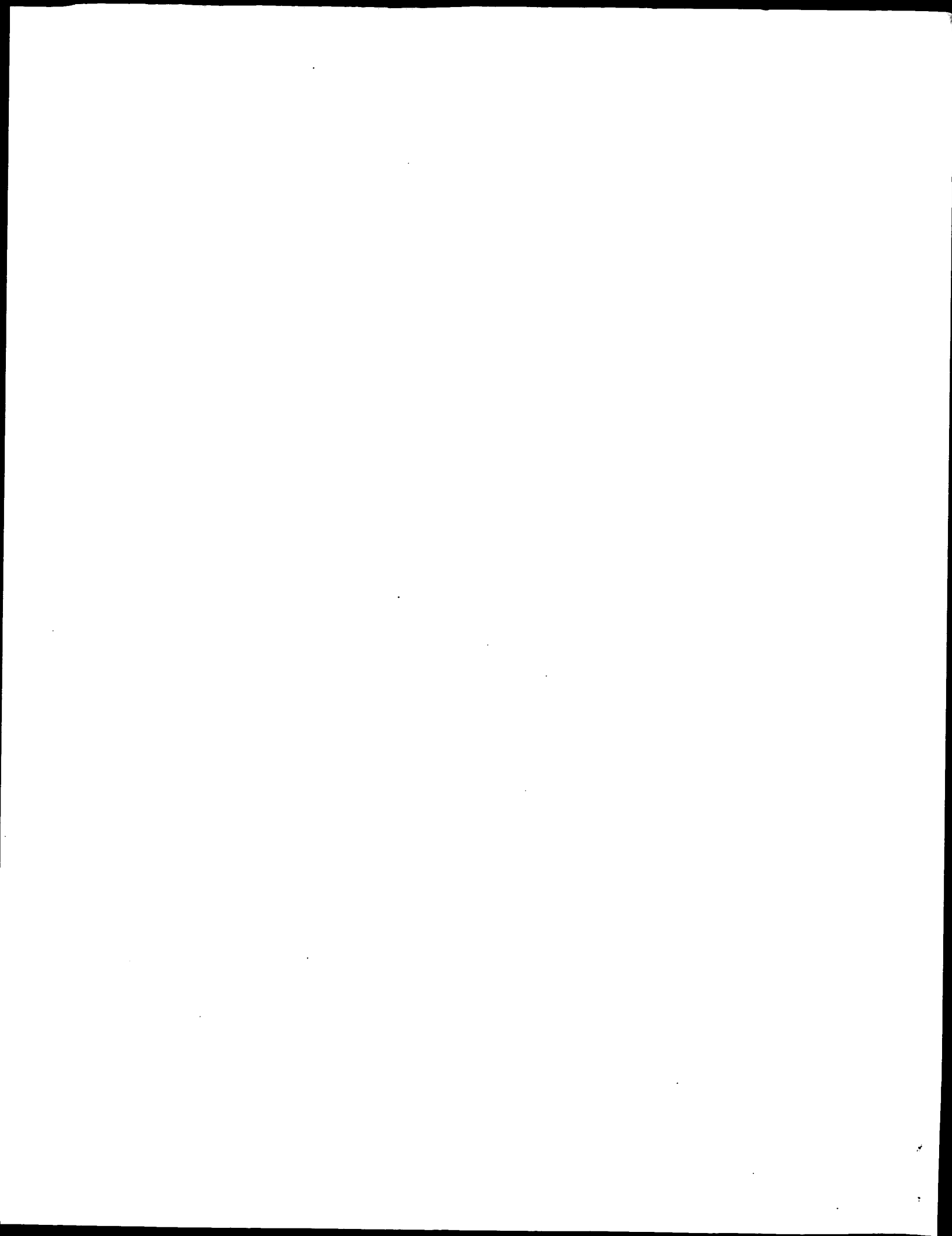
Fri Dec 28 09:12:30 2001

BASE COUNT 50377 a 30527 c 30882 g 45639 t 100 others
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.08;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaaa 1173
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Db 77674 TTATTTCAAAAAAAAAAAAAA 77698

Search completed: December 27, 2001, 16:24:57
Job time: 5749 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 27, 2001, 14:49:08 ; Search time 169.67 Seconds
(without alignments)
5927.050 Million cell updates/sec

Title: US-09-435-054-1
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 930621 seqs, 428662619 residues

Word size : 10

Total number of hits satisfying chosen parameters: 367515

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : N_Geneseq_1101.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1173	100.0	1173	21	MAIZE LEC1 # 1 cod
2	47	4.0	1098	21	Wheat LEC1 # 3 cod
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4	39	3.3	763	21	Maize LEC1 # 2 cod
5	32	2.7	1121	21	Soybean LEC1 # 2 c
6	26	2.2	796	21	Soybean LEC1 # 3 c
7	25	2.1	417	21	Cat flea hindgut a
8	25	2.1	417	21	Cat flea hindgut a
9	25	2.1	1234	21	Soybean neutral tr
10	25	2.1	4590	7	Sequence encoding
11	24	2.0	36	21	Reverse PCR primer

12	24	2.0	500	19	AAV73459	Flea saliva protei
13	24	2.0	500	19	AAV73460	Flea saliva protei
14	24	2.0	653	22	AAH87686	Peppermint plant o
15	24	2.0	886	21	AAH59457	Nucleotide sequenc
16	24	2.0	886	21	AAH53393	Clone se.127b04 nu
17	24	2.0	886	21	AAH53393	Soybean glutathion
18	24	2.0	886	21	AAH53393	Soybean type I GST
19	24	2.0	1231	21	AAH53393	Maize replication
20	24	2.0	1316	22	AAH55043	Nucleotide sequenc
21	24	2.0	1372	22	AAH24830	Nucleotide sequenc
22	24	2.0	1372	22	AAH24831	Nucleotide sequenc
23	24	2.0	1399	21	AAH16022	Human prostate can
24	24	2.0	1466	20	AAH25133	Human hypoxia indu
25	24	2.0	1466	22	AAH03429	Human hypoxia indu
26	24	2.0	1928	22	AAH09829	Soybean SPFI-relat
27	24	2.0	2254	21	AAH59457	Human secreted pro
28	24	2.0	2327	12	AAH12152	Human transferrin
29	24	2.0	2327	21	AAH24196	Human serum trans
30	24	2.0	2993	20	AAH76374	Pneumocystis carin
31	23	2.0	24	20	AAH00877	PCR primer PGR732
32	23	2.0	42	16	AAH06155	Sindbis polyA prim
33	23	2.0	42	17	AAH35054	Sindbis virus stra
34	23	2.0	42	17	AAH30789	Sindbis genomic CD
35	23	2.0	42	19	AAH60127	PCR primer 4B used
36	23	2.0	42	19	AAH60127	PCR primer 4B used
37	23	2.0	42	20	AAH70686	Primer 4B used to
38	23	2.0	42	21	AAH292767	Sindbis virus geno
39	23	2.0	42	21	AAH292894	Sindbis virus geno
40	23	2.0	48	16	AAH06183	Primer SINKball700
41	23	2.0	48	17	AAH35073	Sindbis-based, tum
42	23	2.0	48	17	AAH30807	Sindbis PCR primer
43	23	2.0	48	19	AAH42384	Reverse PCR primer
44	23	2.0	48	20	AAH70704	Reverse PCR primer
45	23	2.0	48	21	AAH292785	Sindbis basic vect
46	23	2.0	48	21	AAH292912	Sindbis basic vect
47	23	2.0	52	18	AAH59252	Primer 4B used SIN
48	23	2.0	52	18	AAH59252	Primer 4B used SIN
49	23	2.0	58	18	AAH59240	Primer 11,703R use
50	23	2.0	58	20	AAH59482	Reverse primer SIN
51	23	2.0	65	18	AAH59261	Reverse primer SIN
52	23	2.0	65	20	AAH59503	Reverse primer SIN
53	23	2.0	96	19	AAH34417	E. coli lys S gene
54	23	2.0	218	21	AAH98737	Human colon cancer
55	23	2.0	396	22	AAH94839	Human ovarian can
56	23	2.0	401	22	AAH66801	Novel human polynu
57	23	2.0	437	22	AAH12484	Human cDNA clone (
58	23	2.0	612	21	AAH00804	Human irritable bo
59	23	2.0	615	17	AAH18233	Prepro-FALI-99 CDN
60	23	2.0	683	20	AAH61461	DNA encoding a hum
61	23	2.0	733	21	AAH59839	Human secreted pro
62	23	2.0	753	20	AAH87413	Hepatocellular car
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64	23	2.0	760	20	AAH76970	Histamine binding
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72	23	2.0	1049	21	AAH15600	Nucleotide sequenc
73	23	2.0	1095	20	AAH30366	Human prostate can
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81	23	2.0	1506	17	AAH95302	Murine Fas antigen
82	23	2.0	1506	16	AAH16305	Coding sequence fo
83	23	2.0	1506	20	AAH71961	Fas ligand (FasL)
84	23	2.0	1531	21	AAH97040	Human secreted pro

85	23	2.0	1532	20	AA117762	Stereoselective es	c 158	22	1.9	256	21	AA16382	Human colon cancer
86	23	2.0	1550	21	AA57955	1550 bp Candida al	c 159	22	1.9	262	20	AAV89954	EST clone CS682
87	23	2.0	1613	20	AA230704	Ret neuronal immed	c 160	22	1.9	321	22	AA163754	Human kidney relat
88	23	2.0	1747	21	AA98129	Human colon cancer	c 161	22	1.9	336	21	AA16503	Human colon cancer
89	23	2.0	1748	20	AA08944	Fragment of human	c 162	22	1.9	351	21	AA56526	Eucalyptus grandis
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91	23	2.0	1963	13	AA51400	Chromosome 16q tum	c 164	22	1.9	369	21	AA311283	Plant microsatellit
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99	23	2.0	2300	18	AA762735	Herbicide-resistan	c 172	22	1.9	393	21	AA565934	Human prostate can
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105	23	2.0	2319	13	AAQ22539	KDI-341 DNA. Sind	c 178	22	1.9	438	18	AAV00425	Human colon cancer
106	23	2.0	2335	13	AAQ22538	KDI-325 DNA. Sind	c 179	22	1.9	438	18	AAV00425	Human secreted pro
107	23	2.0	2353	13	AAQ22537	KDI-507 cDNA. Sin	c 180	22	1.9	439	22	AA565685	Human 559-41 secre
108	23	2.0	2360	13	AAQ22536	DI-25 cDNA. Sindb	c 181	22	1.9	439	22	AA565685	3' fragment of clo
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110	23	2.0	2435	19	AAV64580	Tobacco chld DNA.	c 183	22	1.9	507	20	AA303331	Plant microsatelli
111	23	2.0	2535	21	AA718128	Lung cancer associ	c 184	22	1.9	507	20	AA303331	Soybean cysteine p
112	23	2.0	2566	22	AA746555	Mouse intracellular	c 185	22	1.9	549	21	AA565219	Human secreted pro
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119	23	2.0	7970	21	AA903489	Plasmid pH-BB DNA	c 192	22	1.9	577	21	AA16198	Human breast cancer
120	23	2.0	9542	20	AA77359	Polynucleotide seq	c 193	22	1.9	581	20	AA81761	Human cDNA clone
121	23	2.0	9542	21	AA90391	987BBneo DNA seque	c 194	22	1.9	581	20	AA81761	Trypanosoma cruzi
122	23	2.0	9542	21	AA90391	Polynucleotide seq	c 195	22	1.9	581	20	AA81761	DNA encoding a T.
123	23	2.0	9551	21	AA77354	Polynucleotide seq	c 196	22	1.9	581	20	AA81761	Pinus radiata cell
124	23	2.0	9551	21	AA90386	Sindbis expression	c 197	22	1.9	581	20	AA81761	DNA encoding sugar
125	23	2.0	9551	21	AA90386	Alphaviral vector	c 198	22	1.9	581	20	AA81761	Human colon cancer
126	23	2.0	10524	20	AA77355	Polynucleotide seq	c 199	22	1.9	581	20	AA81761	E-Dex integrin inh
127	23	2.0	10524	21	AA90387	Complete cDNA sequ	c 200	22	1.9	595	17	AA16988	Human cancer assoc
128	23	2.0	11282	20	AA77354	Alphaviral vector	c 201	22	1.9	604	21	AA77881	Human secreted pro
129	23	2.0	11282	22	AA77354	Human genomic DNA	c 202	22	1.9	604	21	AA77881	Human secreted pro
130	23	2.0	11282	22	AA77354	Polynucleotide seq	c 203	22	1.9	604	21	AA77881	Human secreted pro
131	23	2.0	11617	22	AA77356	Polynucleotide seq	c 204	22	1.9	604	21	AA77881	Human secreted pro
132	23	2.0	11927	21	AA90388	Plasmid pSinp5 h	c 205	22	1.9	604	21	AA77881	Human secreted pro
133	23	2.0	13905	20	AA77358	Polynucleotide seq	c 206	22	1.9	604	21	AA77881	Human secreted pro
134	23	2.0	13905	20	AA90390	Plasmid pT5'2J DN	c 207	22	1.9	604	21	AA77881	Human secreted pro
135	23	2.0	16656	16	AAQ86154	Eukaryotic layered	c 208	22	1.9	604	21	AA77881	Human secreted pro
136	23	2.0	16656	17	AA730787	Alphavirus-based e	c 209	22	1.9	604	21	AA77881	Human secreted pro
137	23	2.0	16656	19	AAV60125	Representative euk	c 210	22	1.9	604	21	AA77881	Human secreted pro
138	23	2.0	16656	19	AAV42304	Representative euk	c 211	22	1.9	604	21	AA77881	Human secreted pro
139	23	2.0	16656	20	AAV70684	Representative euk	c 212	22	1.9	604	21	AA77881	Human secreted pro
140	23	2.0	16656	21	AA292765	Representative euk	c 213	22	1.9	604	21	AA77881	Human secreted pro
141	23	2.0	16656	21	AA292892	Representative euk	c 214	22	1.9	604	21	AA77881	Human secreted pro
142	23	2.0	45186	22	AA560478	Wild-type human CT	c 215	22	1.9	604	21	AA77881	Human secreted pro
143	23	2.0	119950	20	AA50201	Human ves1 gene.	c 216	22	1.9	604	21	AA77881	Human secreted pro
144	23	2.0	235033	19	AAV57926	Hereditary haemoch	c 217	22	1.9	604	21	AA77881	Human secreted pro
145	23	2.0	237326	19	AAV57903	Hereditary haemoch	c 218	22	1.9	604	21	AA77881	Human secreted pro
146	23	2.0	237326	20	AAV57903	LEC1 primer # 6.	c 219	22	1.9	604	21	AA77881	Human secreted pro
147	23	2.0	237326	21	AAV57903	Western equine enc	c 220	22	1.9	604	21	AA77881	Human secreted pro
148	23	2.0	237326	22	AAV57903	Western equine enc	c 221	22	1.9	604	21	AA77881	Human secreted pro
149	23	2.0	237326	23	AAV57903	Western equine enc	c 222	22	1.9	604	21	AA77881	Human secreted pro
150	23	2.0	237326	24	AAV57903	Western equine enc	c 223	22	1.9	604	21	AA77881	Human secreted pro
151	23	2.0	237326	25	AAV57903	Western equine enc	c 224	22	1.9	604	21	AA77881	Human secreted pro
152	23	2.0	237326	26	AAV57903	Western equine enc	c 225	22	1.9	604	21	AA77881	Human secreted pro
153	23	2.0	237326	27	AAV57903	Western equine enc	c 226	22	1.9	604	21	AA77881	Human secreted pro
154	23	2.0	237326	28	AAV57903	Western equine enc	c 227	22	1.9	604	21	AA77881	Human secreted pro
155	23	2.0	237326	29	AAV57903	Western equine enc	c 228	22	1.9	604	21	AA77881	Human secreted pro
156	23	2.0	237326	30	AAV57903	Western equine enc	c 229	22	1.9	604	21	AA77881	Human secreted pro
157	23	2.0	237326	31	AAV57903	Western equine enc	c 230	22	1.9	604	21	AA77881	Human secreted pro

231	22	1.9	860	20	AAV81622	Arabisopsis PR-1 p	304	22	1.9	1751	19	AAV29518	Human TRAIL polype
232	22	1.9	886	20	AAV51754	DNA encoding a hum	305	22	1.9	1769	19	AAV63096	Human TL2 CDNA. H
233	22	1.9	894	20	AAV99723	Human adult retina	306	22	1.9	1769	21	AAV64325	DNA encoding a hum
234	22	1.9	919	21	AAV95527	Human secreted pro	307	22	1.9	1769	22	AAV64745	Human TL2 polypept
235	22	1.9	930	20	AAV06256	Human secreted pro	308	22	1.9	1781	20	AAV02969	Human IL-1ra BAC c
236	22	1.9	939	22	AAV03897	Human secreted pro	309	22	1.9	1803	20	AAV63447	Human ADAMTS-R1 cD
237	22	1.9	963	21	AAV33117	Human secreted pro	310	22	1.9	1806	22	AAV74203	DNA encoding eviro
238	22	1.9	965	21	AAV07675	Fusarium venenatum	311	22	1.9	1819	22	AAH34836	Human colon cancer
239	22	1.9	1007	21	AAV59458	Nucleotide sequenc	312	22	1.9	1848	22	AAH33307	Human colon cancer
240	22	1.9	1007	21	AAV53394	Clone sm.pk0026.g	313	22	1.9	1849	21	AAH33307	Human cancer assoc
241	22	1.9	1007	22	AAV294950	Soybean glutathion	314	22	1.9	1869	21	AAV52775	Human cancer assoc
242	22	1.9	1007	22	AAV31573	Soybean type II GS	315	22	1.9	1877	21	AAV52775	Soybean putative c
243	22	1.9	1018	20	AAV51723	DNA encoding a hum	316	22	1.9	1882	22	AAV63442	Human secreted pro
244	22	1.9	1020	21	AAV74306	Human secreted pro	317	22	1.9	1882	22	AAV02471	CDNA clone bshl.pk
245	22	1.9	1069	22	AAH33555	Human colon cancer	318	22	1.9	1897	19	AAV16291	Arabidopsis thalia
246	22	1.9	1100	22	AAV59119	Nucleotide sequenc	319	22	1.9	1920	21	AAV59071	Human secreted pro
247	22	1.9	1104	22	AAV01165	Fertilisation inde	320	22	1.9	1926	20	AAV21254	Human growth-relat
248	22	1.9	1121	22	AAV97943	Human secreted pro	321	22	1.9	1926	20	AAV79500	Human growth-relat
249	22	1.9	1144	19	AAV59628	Human secreted pro	322	22	1.9	1932	21	AAV26444	Human secreted pro
250	22	1.9	1149	21	AAV27933	Human secreted pro	323	22	1.9	1932	21	AAV26444	Human secreted pro
251	22	1.9	1175	21	AAV18303	Soybean phosphatid	324	22	1.9	1932	21	AAV59531	Human secreted pro
252	22	1.9	1193	21	AAV16156	Lung cancer associ	325	22	1.9	2002	19	AAV36503	Human D2-2 gene as
253	22	1.9	1202	20	AAV52858	Human prostate can	326	22	1.9	2012	22	AAH8913	Endometrial bleedi
254	22	1.9	1210	22	AAV26564	DNA encoding hum	327	22	1.9	2025	20	AAH81876	Sweetgum 4-coumar
255	22	1.9	1226	20	AAV24897	Human secreted pro	328	22	1.9	2025	21	AAH81876	DNA encoding a Cou
256	22	1.9	1243	21	AAV59453	Human secreted pro	329	22	1.9	2047	22	AAV37900	L. styraciflua ang
257	22	1.9	1252	21	AAV46413	Human secreted pro	330	22	1.9	2100	21	AAV59531	Mouse Wnt-inhibito
258	22	1.9	1258	22	AAV10108	CDNA encoding a ly	331	22	1.9	2100	21	AAV59531	Human secreted pro
259	22	1.9	1270	15	AAV65859	Mouse ZCYT07 CDNA	332	22	1.9	2103	22	AAV08708	Human secreted pro
260	22	1.9	1280	19	AAV28525	Wheat leaf ADP-glu	333	22	1.9	2116	18	AAV99541	Lycopersicon penne
261	22	1.9	1287	21	AAV89936	Blackcurrant rever	334	22	1.9	2168	20	AAV73485	Human hyaluronan s
262	22	1.9	1315	20	AAV241312	Arabidopsis NAC1 D	335	22	1.9	2182	19	AAV00731	Human SRE-2BP anal
263	22	1.9	1320	22	AAV23895	Human normal ovari	336	22	1.9	2206	20	AAV22781	Pea plastidial pho
264	22	1.9	1332	19	AAV40647	Human secreted pro	337	22	1.9	2206	20	AAV22781	Human SOCS19 CDNA
265	22	1.9	1332	20	AAV02709	Human transaldolas	338	22	1.9	2251	21	AAV50895	Human SOCS19 CDNA
266	22	1.9	1332	21	AAV257576	Human transaldolas	339	22	1.9	2252	22	AAH16606	Soybean phosphatid
267	22	1.9	1362	21	AAV69101	Human secreted pro	340	22	1.9	2272	17	AAH11104	Transforming growt
268	22	1.9	1363	20	AAV00449	Human secreted pro	341	22	1.9	2346	21	AAV74421	Human TGF-beta M1
269	22	1.9	1367	21	AAV18188	Human secreted pro	342	22	1.9	2352	21	AAV59895	Human cancer assoc
270	22	1.9	1368	20	AAV06262	Lung cancer associ	343	22	1.9	2352	21	AAV59895	Human secreted pro
271	22	1.9	1369	20	AAV84974	Human secreted pro	344	22	1.9	2381	15	AAV068910	Human c-myc far up
272	22	1.9	1373	21	AAV77739	Human secreted pro	345	22	1.9	2389	21	AAV61893	Human c-myc far up
273	22	1.9	1404	16	AAV34680	Human cancer assoc	346	22	1.9	2393	20	AAV21093	CDNA encoding a hu
274	22	1.9	1406	21	AAV95793	Medium chain-speci	347	22	1.9	2406	21	AAV22407	Human secreted pro
275	22	1.9	1453	22	AAV34186	Apoptosis related	348	22	1.9	2412	21	AAV69103	Human secreted pro
276	22	1.9	1466	20	AAV98009	Human colon cancer	349	22	1.9	2432	21	AAV78180	Human secreted pro
277	22	1.9	1481	22	AAV95076	Human secreted pro	350	22	1.9	2503	21	AAV69461	Human cancer assoc
278	22	1.9	1484	21	AAV15813	Nucleotide sequenc	351	22	1.9	2528	22	AAH72703	Human secreted pro
279	22	1.9	1495	21	AAV55201	Human prostate can	352	22	1.9	2550	22	AAV74283	Human cervical can
280	22	1.9	1495	22	AAV08502	Human secreted pro	353	22	1.9	2590	21	AAV36239	Cucurbita pepo cal
281	22	1.9	1501	21	AAV75917	Human secreted pro	354	22	1.9	2650	17	AAV07328	CDNA encoding a bo
282	22	1.9	1505	20	AAV41298	Human normal ovari	355	22	1.9	2658	20	AAV07196	Human PH30 beta ch
283	22	1.9	1521	20	AAV73000	Human foetal ovari	356	22	1.9	2668	21	AAV79150	Human lung tumour
284	22	1.9	1540	9	AAV80917	Sequence of the 3'	357	22	1.9	2718	22	AAV79919	Human lung tumour
285	22	1.9	1541	21	AAV27924	Maize Rad2/FEN-1 c	358	22	1.9	2735	22	AAH16242	Nucleotide sequenc
286	22	1.9	1543	22	AAH13689	Human CDNA sequenc	359	22	1.9	2737	21	AAV64478	Human CDNA sequenc
287	22	1.9	1544	18	AAV90731	Human placental bi	360	22	1.9	2769	21	AAV64478	Human H3087 (clon
288	22	1.9	1544	21	AAV70406	Human placental bi	361	22	1.9	2786	22	AAH34862	Human ORFX ORF1940
289	22	1.9	1546	22	AAV69116	Human secreted pro	362	22	1.9	2802	21	AAV7151	Human colon cancer
290	22	1.9	1560	22	AAV31049	Abscisic acid-acti	363	22	1.9	2805	22	AAH32551	Human corticollber
291	22	1.9	1575	18	AAV91305	Human J59-41 secre	364	22	1.9	2835	19	AAV58755	Human breast and o
292	22	1.9	1576	21	AAV51347	z. mays sucrose no	365	22	1.9	2850	22	AAH32551	Human secreted pro
293	22	1.9	1610	19	AAV33063	Human tissue facto	366	22	1.9	2908	21	AAV58755	Human secreted pro
294	22	1.9	1643	21	AAV69117	Human secreted pro	367	22	1.9	2922	12	AAQ13675	Human secreted pro
295	22	1.9	1646	19	AAV18016	Pinus radiata cone	368	22	1.9	3014	22	AAH73988	E2A/prl fusion tra
296	22	1.9	1647	13	AAQ21621	Human Tryptophan-2	369	22	1.9	3039	21	AAV21851	Human corticollber
297	22	1.9	1671	20	AAV30705	Rat neuronal immed	370	22	1.9	3076	20	AAV73003	Human adult brain
298	22	1.9	1687	21	AAV59951	Human secreted pro	371	22	1.9	3095	22	AAV44823	RPP5-like protein
299	22	1.9	1692	22	AAH32543	Human secreted pro	372	22	1.9	3103	21	AAV44823	Sucrose synthase p
300	22	1.9	1693	21	AAV78013	Human cancer associ	373	22	1.9	3117	21	AAV18178	Lung cancer associ
301	22	1.9	1697	22	AAV33051	Human secreted pro	374	22	1.9	3192	22	AAV21281	Human CDNA sequenc
302	22	1.9	1731	22	AAH81783	Human secreted pro	375	22	1.9	3260	22	AAV58331	Human GTP-binding
303	22	1.9	1751	18	AAV72847	Human differential	376	22	1.9	3307	22	AAH43167	LPD-599. Syntheti
	22	1.9				Human apoptosis in	377	22	1.9	3311	17	AAV10562	Alpha-amylase gene
	22	1.9					378	22	1.9	3311	19	AAV61458	Alpha-amylase amya

377	22	1.9	3442	13	AAQ21623	Human Tryptophan O	450	21	1.8	389	21	AAC94591	Cat flea hindgut a
378	22	1.9	3629	19	AAQ26289	Human secreted pro	451	21	1.8	389	22	AAF66032	Novel human polynu
379	22	1.9	4253	21	AAV40888	Coding sequence of	c 452	21	1.8	391	17	AAI12184	Partial pJG4-5-CDK
380	22	1.9	4253	21	AAQ44156	Nucleotide sequenc	c 453	21	1.8	392	17	AAI12197	CDK4 binding prote
381	22	1.9	4253	21	AAQ98453	Human CDNA clone A	c 454	21	1.8	409	21	AAA43737	Mouse secreted exp
382	22	1.9	4457	21	AAQ75360	Human ORFX ORF915	c 455	21	1.8	419	22	AAF66382	Novel human polynu
383	22	1.9	5696	20	AAQ37304	Human hTLP2 CDNA	c 456	21	1.8	426	22	AAH72979	Human cervical can
384	22	1.9	6107	21	AAQ298053	Human secreted pro	c 457	21	1.8	432	21	AAC59323	Human secreted pro
385	22	1.9	6107	22	AAAD11666	Human secreted pro	c 458	21	1.8	434	20	AAQ30386	DNA encoding a hum
386	22	1.9	6430	20	AAQ022992	Human II-lra BAC c	c 459	21	1.8	434	20	AAQ30386	Maize indole-3-gl
387	22	1.9	7432	19	AAV61459	Vector pPR70 conta	c 460	21	1.8	454	20	AAZ22858	Cat flea hindgut a
388	22	1.9	7498	21	AAQ63786	Nucleotide sequenc	c 461	21	1.8	454	20	AAZ22858	cDNA encoding the
389	22	1.9	16225	22	AAI62650	Human breast or ov	c 462	21	1.8	455	21	AAC94914	DNA encoding a hum
390	22	1.9	32152	22	AAI57791	Human colorectal c	c 463	21	1.8	455	19	AAV38429	probe #1804 used t
391	22	1.9	42881	22	AAQ97868	Human neuroblastom	c 464	21	1.8	471	22	AAI33201	probe #1804 used t
392	22	1.9	49999	20	AAZ233903	Human LOBO homolog	c 465	21	1.8	471	22	AAI01813	Arabidopsis thalia
393	22	1.9	56516	20	AAQ00870	Human c-fms oncoge	c 466	21	1.8	487	21	AAC32641	Human colon cancer
394	22	1.9	56520	20	AAQ01022	Wild type PGI codi	c 467	21	1.8	487	22	AAH34982	Human colon cancer
395	22	1.9	66566	20	AAQ53450	Human thioedoxin	c 468	21	1.8	488	21	AAA16466	Cat flea hindgut a
396	22	1.9	66885	22	AAQ07280	Human genomic DNA	c 469	21	1.8	496	21	AAC93977	Human secreted pro
397	22	1.9	160552	22	AAQ02697	Human glycosyl sul	c 470	21	1.8	497	21	AAC99925	Human CDNA clone (
398	22	1.9	163319	21	AAQ22306	Arabidopsis thalia	c 471	21	1.8	506	22	AAH06013	Human secreted pro
399	22	1.9	319608	21	AAH51601	Human chromosome 1	c 472	21	1.8	545	21	AAC63443	Cat flea hindgut a
400	22	1.9	319608	22	AAQ09301	Human schizophre	c 473	21	1.8	545	21	AAC63443	Human prostate can
401	22	1.9	319608	21	AAQ09301	Reverse transcript	c 474	21	1.8	553	22	AAI18729	probe #8662 for ge
402	21	1.8	27	22	AAH43080	Nucleotide sequenc	c 475	21	1.8	562	22	AAI18729	probe #12524 used
403	21	1.8	30	17	AAI15272	Asci-HindIII gene	c 476	21	1.8	562	22	AAI18729	Parietaria allerger
404	21	1.8	34	18	AAI1288	Polyhistidine tail	c 477	21	1.8	568	17	AAI29004	DNA encoding a hum
405	21	1.8	54	15	AAI15573	Primer for HIV RNA	c 478	21	1.8	570	20	AAV55016	Fragment of GABA 9
406	21	1.8	64	15	AAQ68613	trNAPOLYU primer #	c 479	21	1.8	575	19	AAV55016	Polynucleotide cto
407	21	1.8	76	18	AAQ90806	Mouse persepchin ge	c 480	21	1.8	575	20	AAV55016	Fusarium venenatum
408	21	1.8	76	20	AAQ60475	Probe #17639 for g	c 481	21	1.8	582	21	AAQ9836	Human secreted pro
409	21	1.8	155	22	AAI27706	Probe #25357 used	c 482	21	1.8	582	21	AAQ9836	Pathogen response
410	21	1.8	184	22	AAH22416	Mouse hexokinase I	c 483	21	1.8	585	22	AAI1573	Human CDNA encodin
411	21	1.8	236	22	AAH72201	Human cervical can	c 484	21	1.8	588	21	AAQ08885	Fusarium venenatum
412	21	1.8	244	21	AAQ55136	Human secreted pro	c 485	21	1.8	597	20	AAQ37486	Human colon cancer
413	21	1.8	244	21	AAQ55136	Arabidopsis thalia	c 486	21	1.8	599	20	AAQ37486	Human colon cancer
414	21	1.8	248	21	AAQ59297	Cat flea head and	c 487	21	1.8	601	20	AAQ37498	Human secreted pro
415	21	1.8	270	21	AAH31441	Plant microsatelli	c 488	21	1.8	604	21	AAQ30307	Human colon cancer
416	21	1.8	270	21	AAH31441	Human cervical can	c 489	21	1.8	620	21	AAQ55287	Soybean cyclin-dep
417	21	1.8	270	22	AAH71139	Human secreted pro	c 490	21	1.8	629	20	AAV80672	Partial human DNAX
418	21	1.8	276	22	AAH69336	Cervical cancer pr	c 491	21	1.8	636	22	AAQ82509	Human breast tumou
419	21	1.8	282	22	AAQ07747	Human cervical can	c 492	21	1.8	640	21	AAQ77642	Human cancer assoc
420	21	1.8	296	21	AAQ00871	Human colon cancer	c 493	21	1.8	640	22	AAC84350	Corn clone 7001028
421	21	1.8	304	21	AAQ81715	Human secreted pro	c 494	21	1.8	641	21	AAQ74283	Human CDNA clone (
422	21	1.8	307	22	AAH72404	Human cervical can	c 495	21	1.8	645	22	AAQ08373	Human CDNA clone (
423	21	1.8	311	22	AAQ99965	Human secreted pro	c 496	21	1.8	648	21	AAQ77521	Human ORFX ORF3076
424	21	1.8	325	21	AAQ99965	Human secreted pro	c 497	21	1.8	655	22	AAQ44481	Mouse dextran sod1
425	21	1.8	331	22	AAH69518	Human secreted pro	c 498	21	1.8	658	20	AAQ99100	Human cancer cell
426	21	1.8	340	22	AAH87797	Peppermint plant o	c 499	21	1.8	658	21	AAC95532	Human secreted pro
427	21	1.8	345	22	AAH33454	Human colon cancer	c 500	21	1.8	672	22	AAQ11574	Human secreted pro
428	21	1.8	345	22	AAH33454	Cat flea hindgut a	c 501	21	1.8	672	22	AAQ11574	Human secreted pro
429	21	1.8	348	21	AAQ94880	Novel human polynu	c 502	21	1.8	675	21	AAH70110	Human secreted pro
430	21	1.8	368	22	AAQ64984	Peppermint plant o	c 503	21	1.8	675	22	AAH70110	Human secreted pro
431	21	1.8	372	22	AAH88004	Human secreted pro	c 504	21	1.8	676	22	AAQ61318	A. thaliana psae1
432	21	1.8	376	21	AAQ15926	Human secreted pro	c 505	21	1.8	684	15	AAQ72956	DNA encoding a hum
433	21	1.8	378	21	AAQ74350	Human 10 kb Clara	c 506	21	1.8	684	20	AAQ30351	Rat progression re
434	21	1.8	378	22	AAQ91758	Novel human polynu	c 507	21	1.8	687	20	AAQ90807	Strawberry alcohol
435	21	1.8	382	22	AAQ64646	cDNA sequence of p	c 508	21	1.8	694	21	AAQ64777	Strawberry alcohol
436	21	1.8	383	19	AAV61297	Prostate tumour sp	c 509	21	1.8	694	21	AAQ27677	Human colon cancer
437	21	1.8	383	19	AAV58559	Human immunogenic	c 510	21	1.8	694	21	AAQ27677	Human secreted pro
438	21	1.8	383	21	AAQ06322	Human prostate tum	c 511	21	1.8	698	21	AAQ84623	Human secreted pro
439	21	1.8	383	22	AAQ10081	Human prostate-spe	c 512	21	1.8	707	20	AAV84623	Human secreted pro
440	21	1.8	383	22	AAH93438	Human prostate-spe	c 513	21	1.8	723	18	AAC44453	Arabidopsis thalia
441	21	1.8	383	22	AAH84752	Prostate tumour an	c 514	21	1.8	723	18	AAC44453	Soybean albumin 1
442	21	1.8	383	22	AAH02503	Extended cDNA sequ	c 515	21	1.8	723	18	AAC44453	Human cervical can
443	21	1.8	384	19	AAV61328	Prostate tumour sp	c 516	21	1.8	732	22	AAI13385	Human secreted pro
444	21	1.8	384	19	AAV58653	Human immunogenic	c 517	21	1.8	732	22	AAI13385	Human secreted pro
445	21	1.8	384	21	AAQ06416	Human prostate tum	c 518	21	1.8	737	18	AAQ78498	Dirofilaria immiti
446	21	1.8	384	22	AAQ10175	Human prostate-spe	c 519	21	1.8	737	18	AAQ78498	Dirofilaria immiti
447	21	1.8	384	22	AAH93532	Human prostate-spe	c 520	21	1.8	739	21	AAC95547	Human secreted pro
448	21	1.8	384	22	AAH84846	Prostate tumour an	c 521	21	1.8	741	21	AAQ26293	Human secreted pro
449	21	1.8	384	22	AAH02597	Prostate tumour an	c 522	21	1.8	742	13	AAQ22005	Sequence encoding
										745	20	AAQ04338	Human secreted pro

523	1.8	747	21	AA12354	Aspergillus oryzae	596	21	1.8	1063	19	AA11154	Human EST cDNA. H
524	1.8	750	21	AA01845	Human colon cancer	597	21	1.8	1063	19	AA12466	Human oestrogen su
525	1.8	769	21	AA09474	Human secreted pro	598	21	1.8	1072	21	AA04137	Nucleotide sequenc
526	1.8	770	21	AA05232	Human secreted pro	599	21	1.8	1074	19	AA02387	Plant OMT enzyme D
527	1.8	771	21	AA01647	Human gene express	600	21	1.8	1074	20	AA02687	Pine O-methyl tran
528	1.8	772	21	AA04481	Human breast cance	601	21	1.8	1074	21	AA06796	Pinus radiata OMT
529	1.8	779	21	AA01619	Human prostate can	602	21	1.8	1075	19	AA02387	Plant OMT enzyme D
530	1.8	780	21	AA05912	Human transcrip tio	603	21	1.8	1075	20	AA02687	Pine O-methyl tran
531	1.8	781	21	AA01566	Human gene express	604	21	1.8	1075	21	AA06796	Pinus radiata OMT
532	1.8	782	21	AA08095	Human cDNA clone H	605	21	1.8	1082	22	AA01533	Nucleic acid encod
533	1.8	792	21	AA08095	Human cDNA clone H	606	21	1.8	1082	22	AA02648	Human secreted pro
534	1.8	801	21	AA01855	Human cervical can	607	21	1.8	1092	22	AA03137	Human secreted pro
535	1.8	803	21	AA01855	Human colon cancer	608	21	1.8	1094	21	AA05945	Human secreted pro
536	1.8	804	21	AA06147	DNA encoding a hum	609	21	1.8	1100	22	AA05225	Protein PRO303 cDN
537	1.8	808	21	AA04314	Human secreted pro	610	21	1.8	1100	22	AA07247	Human secreted pro
538	1.8	810	21	AA07997	Human secreted pro	611	21	1.8	1104	21	AA06908	Human secreted pro
539	1.8	817	21	AA02443	Human bladder tumo	612	21	1.8	1110	22	AA08972	Maize ZmGnsN1-4 g1
540	1.8	820	19	AA03516	Thuga plicata diri	613	21	1.8	1112	21	AA01389	Aspergillus oryzae
541	1.8	820	22	AA01250	Thuja plicata diri	614	21	1.8	1117	19	AA05911	Nucleotide sequenc
542	1.8	822	20	AA03741	Human secreted pro	615	21	1.8	1135	21	AA09343	Human secreted pro
543	1.8	826	20	AA09989	Fragment of aspart	616	21	1.8	1139	9	AA08029	Interleukin 6. A
544	1.8	835	20	AA01579	Human gene express	617	21	1.8	1139	10	AA09025	Interleukin-6. Ho
545	1.8	845	21	AA04956	Maize MLO1 protein	618	21	1.8	1148	20	AA03961	Breast cancer asso
546	1.8	847	21	AA07794	Human cancer assoc	619	21	1.8	1160	20	AA06143	DNA encoding a hum
547	1.8	850	22	AA05576	Human SCN1A genomi	620	21	1.8	1163	20	AA03436	Human fibroblast g
548	1.8	854	21	AA09345	Human secreted pro	621	21	1.8	1181	21	AA09541	Cat flea HNC anoxi
549	1.8	858	19	AA03516	Human secreted pro	622	21	1.8	1181	21	AA09541	Cat flea HNC Aup h
550	1.8	858	22	AA01249	Forsythia dirigent	623	21	1.8	1182	21	AA07842	Human secreted pro
551	1.8	865	20	AA02514	Wheat Type I gluta	624	21	1.8	1196	21	AA02635	Human secreted pro
552	1.8	866	22	AA01335	Human secreted pro	625	21	1.8	1200	21	AA03335	Human secreted pro
553	1.8	866	22	AA01338	Human secreted pro	626	21	1.8	1200	22	AA01586	Human polynucleoti
554	1.8	872	22	AA00763	Human secreted pro	627	21	1.8	1204	22	AA01638	Human polynucleoti
555	1.8	883	20	AA02481	Human secreted pro	628	21	1.8	1205	20	AA02423	Human normal bladd
556	1.8	886	21	AA04588	cDNA encoding a hu	629	21	1.8	1214	22	AA01136	Rice DNA encoding
557	1.8	889	20	AA03750	Human secreted pro	630	21	1.8	1217	20	AA02483	Human secreted pro
558	1.8	893	16	AA09252	P. communis (pear)	631	21	1.8	1227	21	AA07633	Human ORFX ORF194
559	1.8	900	20	AA07548	Maize glutathione-	632	21	1.8	1232	22	AA07985	Vitis cis-prenyltr
560	1.8	901	21	AA02947	Maize class I glut	633	21	1.8	1233	21	AA04515	Rat 20alpha-hydrox
561	1.8	901	21	AA07625	Maize glutathione-	634	21	1.8	1236	19	AA04811	Nucleotide sequenc
562	1.8	902	21	AA08056	Human secreted pro	635	21	1.8	1250	21	AA05905	Human secreted pro
563	1.8	905	21	AA02745	Veronia mespilifol	636	21	1.8	1253	22	AA03429	Human colon cancer
564	1.8	911	21	AA07626	Maize glutathione-	637	21	1.8	1260	22	AA05499	Human secreted pro
565	1.8	920	22	AA06385	Human polynucleoti	638	21	1.8	1263	21	AA09046	Human uncoupling p
566	1.8	921	20	AA02733	Human secreted pro	639	21	1.8	1267	8	AA07086	Sequence of cDNA c
567	1.8	928	20	AA00080	Human secreted pro	640	21	1.8	1267	14	AA03748	Elmeria tenella TA
568	1.8	930	20	AA06643	Human secreted pro	641	21	1.8	1272	21	AA03623	cDNA encoding a bo
569	1.8	935	20	AA01078	Trehalose-6-phosph	642	21	1.8	1273	20	AA00677	Human sperm-specif
570	1.8	935	21	AA06941	Human secreted pro	643	21	1.8	1276	21	AA07426	Human secreted pro
571	1.8	942	10	AA09011	Fish growth hormon	644	21	1.8	1284	12	AA01536	NF-YB. Homo sapie
572	1.8	944	18	AA09159	Calliphora vomitor	645	21	1.8	1286	21	AA05634	Pinus radiata tran
573	1.8	944	12	AA01091	Fish growth hormon	646	21	1.8	1290	21	AA09549	Human secreted pro
574	1.8	951	20	AA08459	Human secreted pro	647	21	1.8	1295	21	AA04019	H. vulgare nicotia
575	1.8	958	21	AA03936	Arabidopsis thalia	648	21	1.8	1311	21	AA02913	Human secreted pro
576	1.8	967	21	AA07627	Maize glutathione-	649	21	1.8	1314	21	AA04019	H. vulgare nicotia
577	1.8	969	22	AA07246	Human prostate can	650	21	1.8	1319	20	AA08611	cDNA encoding a tr
578	1.8	974	20	AA08612	DNA encoding a Tr	651	21	1.8	1325	20	AA08074	Human secreted pro
579	1.8	983	20	AA08444	Human secreted pro	652	21	1.8	1327	22	AA03375	Human colon cancer
580	1.8	999	20	AA08067	Human DNAX toll-li	653	21	1.8	1327	22	AA07864	Human secreted pro
581	1.8	1000	22	AA03256	Human secreted pro	654	21	1.8	1328	22	AA08747	Human secreted pro
582	1.8	1006	21	AA01264	Aspergillus oryzae	655	21	1.8	1328	22	AA06402	cDNA encoding huma
583	1.8	1006	21	AA07762	Human cancer assoc	656	21	1.8	1331	22	AA09176	Sunflower seedling
584	1.8	1008	22	AA01157	Human cDNA encodin	657	21	1.8	1338	15	AA06567	Rabbit zona pelluc
585	1.8	1008	22	AA00240	Human secreted pro	658	21	1.8	1338	20	AA02271	Rabbit zona pelluc
586	1.8	1009	22	AA08952	Human camello 1 (H	659	21	1.8	1338	20	AA06478	Rabbit oocyte zona
587	1.8	1012	20	AA02121	zea mays eIF-4E pr	660	21	1.8	1338	21	AA02964	Rabbit zona pelluc
588	1.8	1015	21	AA05966	Human secreted pro	661	21	1.8	1338	21	AA04625	Rabbit zona pelluc
589	1.8	1018	20	AA06137	DNA encoding a hum	662	21	1.8	1338	21	AA03324	Rabbit zona pelluc
590	1.8	1037	20	AA03015	Human secreted pro	663	21	1.8	1339	21	AA03780	Human secreted pro
591	1.8	1042	21	AA06419	Nucleotide sequenc	664	21	1.8	1339	21	AA09968	Human colon cancer
592	1.8	1046	12	AA01037	Plasmid pMG3C9 use	665	21	1.8	1358	22	AA03867	Pig Interleukin-10
593	1.8	1046	12	AA01037	Mouse Glutamine re	666	21	1.8	1365	16	AA08704	Porcine interleuki
594	1.8	1061	21	AA04744	Human TANGO 221 co	667	21	1.8	1365	16	AA08572	Human prostate can
595	1.8	1062	21	AA08945	Corn branched chai	668	21	1.8	1366	21	AA01621	

669	1.8	1374	21	AAC99077	Human pancreatic c	742	21	1.8	1707	22	AAD05834	Arabidopsis thalia
670	1.8	1379	22	AAD05828	Arabidopsis thalia	743	21	1.8	1707	22	AAF80403	Nucleotide sequenc
671	1.8	1381	22	AAD05964	Sterol C5 desatura	744	21	1.8	1710	22	AAF99953	Nucleotide sequenc
672	1.8	1389	20	AA227067	Original S. tubero	745	21	1.8	1712	21	AAC76982	Human ORFX ORF2537
673	1.8	1391	20	AA227358	Human secreted pro	746	21	1.8	1714	21	AAD05590	Human secreted pro
674	1.8	1392	22	AA227540	Human secreted pro	747	21	1.8	1720	21	AAA39471	Human ADA2 DNA. H
675	1.8	1393	21	AAA59441	Nucleotide sequenc	748	21	1.8	1724	20	AA204442	Human secreted pro
676	1.8	1393	22	AAF63797	Human secreted pro	749	21	1.8	1733	16	AAQ84046	Japonicum allergen
677	1.8	1410	21	AAC98169	Human colon cancer	750	21	1.8	1733	17	AAAT18102	Japan cedar pollen
678	1.8	1410	22	AAH34321	Human colon cancer	751	21	1.8	1733	17	AAA54528	Phytol/prenyltrans
679	1.8	1411	21	AAA26308	Human secreted pro	752	21	1.8	1743	21	AAA37089	Human PRO1337 (UNQ
680	1.8	1420	21	AAAT8510	Plant SDF polynucl	753	21	1.8	1743	21	AAF54367	Primer #140 used i
681	1.8	1425	20	AA22859	Human secreted pro	754	21	1.8	1747	21	AAA93128	Human secreted pro
682	1.8	1428	20	AA224403	Maize myo-inositol	755	21	1.8	1752	21	AA238575	D. farinae mite al
683	1.8	1433	15	AAQ65397	Elm C10:0-acyl car	756	21	1.8	1752	21	AA238576	D. farinae mite al
684	1.8	1433	16	AAQ92306	Elm class II thioe	757	21	1.8	1753	22	AAAS00149	Human cDNA clone H
685	1.8	1433	17	AAAT36108	Elm acyl-ACP thioe	758	21	1.8	1756	21	AAF16318	Human prostate can
686	1.8	1433	19	AAV15230	C10:0-ACP thioe	759	21	1.8	1758	20	AA207159	Human lung tumour
687	1.8	1437	20	AA222859	Maize indole-3-gly	760	21	1.8	1758	21	AA239079	Human lung tumour
688	1.8	1442	19	AA225906	Rat aquaporin-5 en	761	21	1.8	1781	21	AA239079	p33 tumour suppres
689	1.8	1442	20	AA206779	Human sperm-specif	762	21	1.8	1808	22	AAF16342	Human prostate can
690	1.8	1442	20	AA204106	Rat aquaporin-5 en	763	21	1.8	1808	22	AAF16342	Human prostate can
691	1.8	1443	19	AAV69615	Human secreted pro	764	21	1.8	1810	21	AA239187	Human secreted pro
692	1.8	1448	21	AA239796	Human secreted pro	765	21	1.8	1816	20	AA239797	Human prostate tum
693	1.8	1457	21	AA239822	Human secreted pro	766	21	1.8	1821	22	AA239797	Human secreted pro
694	1.8	1459	22	AA239816	Human secreted pro	767	21	1.8	1844	20	AA239797	GABA-gated chlorid
695	1.8	1465	21	AA239814	Human secreted pro	768	21	1.8	1844	21	AA239797	Human prostate can
696	1.8	1467	21	AA239814	Human secreted pro	769	21	1.8	1849	21	AA239797	Human prostate can
697	1.8	1476	21	AA239814	Human secreted pro	770	21	1.8	1849	21	AA239797	Human prostate can
698	1.8	1477	21	AA239814	Human secreted pro	771	21	1.8	1862	21	AA239797	Human prostate can
699	1.8	1477	21	AA239814	Human secreted pro	772	21	1.8	1862	22	AA239797	Human prostate can
700	1.8	1502	20	AA239814	Human secreted pro	773	21	1.8	1873	21	AA239797	Human prostate can
701	1.8	1503	20	AA239814	Human secreted pro	774	21	1.8	1884	22	AA239797	Human prostate can
702	1.8	1504	21	AA239814	Human secreted pro	775	21	1.8	1884	22	AA239797	Human prostate can
703	1.8	1512	21	AA239814	Human secreted pro	776	21	1.8	1892	20	AA239797	Human prostate can
704	1.8	1515	17	AA239814	Human secreted pro	777	21	1.8	1892	21	AA239797	Human prostate can
705	1.8	1515	17	AA239814	Human secreted pro	778	21	1.8	1892	21	AA239797	Human prostate can
706	1.8	1520	21	AA239814	Human secreted pro	779	21	1.8	1892	21	AA239797	Human prostate can
707	1.8	1532	21	AA239814	Human secreted pro	780	21	1.8	1892	21	AA239797	Human prostate can
708	1.8	1532	22	AA239814	Human secreted pro	781	21	1.8	1892	21	AA239797	Human prostate can
709	1.8	1532	22	AA239814	Human secreted pro	782	21	1.8	1892	21	AA239797	Human prostate can
710	1.8	1555	21	AA239814	Human secreted pro	783	21	1.8	1916	22	AA239797	Human prostate can
711	1.8	1556	22	AA239814	Human secreted pro	784	21	1.8	1916	22	AA239797	Human prostate can
712	1.8	1559	20	AA239814	Human secreted pro	785	21	1.8	1916	22	AA239797	Human prostate can
713	1.8	1574	21	AA239814	Human secreted pro	786	21	1.8	1916	22	AA239797	Human prostate can
714	1.8	1574	22	AA239814	Human secreted pro	787	21	1.8	1916	22	AA239797	Human prostate can
715	1.8	1583	21	AA239814	Human secreted pro	788	21	1.8	1916	22	AA239797	Human prostate can
716	1.8	1588	21	AA239814	Human secreted pro	789	21	1.8	1916	22	AA239797	Human prostate can
717	1.8	1598	22	AA239814	Human secreted pro	790	21	1.8	1916	22	AA239797	Human prostate can
718	1.8	1608	21	AA239814	Human secreted pro	791	21	1.8	1916	22	AA239797	Human prostate can
719	1.8	1614	19	AA239814	Human secreted pro	792	21	1.8	1916	22	AA239797	Human prostate can
720	1.8	1614	22	AA239814	Human secreted pro	793	21	1.8	1916	22	AA239797	Human prostate can
721	1.8	1614	22	AA239814	Human secreted pro	794	21	1.8	1916	22	AA239797	Human prostate can
722	1.8	1619	16	AA239814	Human secreted pro	795	21	1.8	1916	22	AA239797	Human prostate can
723	1.8	1619	20	AA239814	Human secreted pro	796	21	1.8	1916	22	AA239797	Human prostate can
724	1.8	1636	15	AA239814	Human secreted pro	797	21	1.8	1916	22	AA239797	Human prostate can
725	1.8	1638	17	AA239814	Human secreted pro	798	21	1.8	1916	22	AA239797	Human prostate can
726	1.8	1638	20	AA239814	Human secreted pro	799	21	1.8	1916	22	AA239797	Human prostate can
727	1.8	1645	21	AA239814	Human secreted pro	800	21	1.8	1916	22	AA239797	Human prostate can
728	1.8	1655	21	AA239814	Human secreted pro	801	21	1.8	1916	22	AA239797	Human prostate can
729	1.8	1655	21	AA239814	Human secreted pro	802	21	1.8	1916	22	AA239797	Human prostate can
730	1.8	1660	17	AA239814	Human secreted pro	803	21	1.8	1916	22	AA239797	Human prostate can
731	1.8	1661	21	AA239814	Human secreted pro	804	21	1.8	1916	22	AA239797	Human prostate can
732	1.8	1662	21	AA239814	Human secreted pro	805	21	1.8	1916	22	AA239797	Human prostate can
733	1.8	1669	22	AA239814	Human secreted pro	806	21	1.8	1916	22	AA239797	Human prostate can
734	1.8	1676	20	AA239814	Human secreted pro	807	21	1.8	1916	22	AA239797	Human prostate can
735	1.8	1680	22	AA239814	Human secreted pro	808	21	1.8	1916	22	AA239797	Human prostate can
736	1.8	1691	21	AA239814	Human secreted pro	809	21	1.8	1916	22	AA239797	Human prostate can
737	1.8	1691	21	AA239814	Human secreted pro	810	21	1.8	1916	22	AA239797	Human prostate can
738	1.8	1697	22	AA239814	Human secreted pro	811	21	1.8	1916	22	AA239797	Human prostate can
739	1.8	1701	19	AA239814	Human secreted pro	812	21	1.8	1916	22	AA239797	Human prostate can
740	1.8	1701	19	AA239814	Human secreted pro	813	21	1.8	1916	22	AA239797	Human prostate can
741	1.8	1702	22	AA239814	Human secreted pro	814	21	1.8	1916	22	AA239797	Human prostate can

815	21	1.8	2119	14	AAQ43853	Sequence of part o	888	21	1.8	2970	22	AAF33249	Human secreted pro
c 816	21	1.8	2135	22	AAQ39216	Arabidopsis thalia	c 889	21	1.8	3034	21	AAQ57984	3034 bp Candida al
817	21	1.8	2142	22	AAQ72840	Secreted protein g	890	21	1.8	3090	20	AAQ89079	Nucleotide sequenc
818	21	1.8	2143	22	AAQ07938	Human secreted pro	891	21	1.8	3090	21	AAQ27033	Human c-bcl CDNA w
819	21	1.8	2154	21	AAQ55156	Arabidopsis thalia	892	21	1.8	3101	19	AAQ32918	Solanum tuberosum
820	21	1.8	2156	20	AAQ10807	Polynucleotide seq	893	21	1.8	3417	21	AAQ70163	Plasmodium falcipa
c 821	21	1.8	2161	19	AAQ07919	Helicobacter pylori	894	21	1.8	3427	21	AAQ67946	Human ORF ORF2501
822	21	1.8	2173	21	AAQ00810	Human irritable bo	c 895	21	1.8	3471	14	AAQ46673	p mySB CDNA clone.
823	21	1.8	2178	22	AAQ98380	Human CDNA clone B	896	21	1.8	3511	21	AAQ96933	Human secreted pro
824	21	1.8	2190	20	AAQ24407	Human bladder tumo	897	21	1.8	3522	22	AAQ07590	Human secreted pro
825	21	1.8	2207	20	AAQ03845	Partial human 7-tr	898	21	1.8	3568	21	AAQ99491	DNA encoding a mai
826	21	1.8	2219	18	AAQ78852	Human cyclin G1 cD	899	21	1.8	3686	22	AAQ85358	Murine SOCS-3 prom
827	21	1.8	2236	21	AAQ00311	Human Ras signalli	900	21	1.8	3693	21	AAQ33335	Human secreted pro
828	21	1.8	2273	22	AAQ162754	Human CDNA SEQ ID	901	21	1.8	3696	22	AAQ72827	Secreted protein g
829	21	1.8	2273	22	AAQ33306	Human colon cancer	902	21	1.8	3707	22	AAQ08367	Human secreted pro
830	21	1.8	2287	21	AAQ69105	Human secreted pro	903	21	1.8	3734	22	AAQ21317	Human CDNA sequenc
831	21	1.8	2287	22	AAQ07819	Human secreted pro	904	21	1.8	3784	11	AAQ05326	Sequence of new pl
832	21	1.8	2288	22	AAQ97897	Human secreted pro	905	21	1.8	3850	9	AAQ81634	Yellow tail tuna DN
833	21	1.8	2294	22	AAQ63419	Human CD39-L2 spli	906	21	1.8	3851	18	AAQ79857	Intron 3 of human
834	21	1.8	2324	21	AAQ48578	CDNA encoding whea	907	21	1.8	3851	18	AAQ79857	Murine SOCS-3 prom
835	21	1.8	2326	20	AAQ85833	DNA encoding human	908	21	1.8	3865	18	AAQ96833	Human PRO1012 nucl
836	21	1.8	2326	20	AAQ31279	Human mammatatin	909	21	1.8	3940	22	AAQ85356	Human PRO1012 (UNQ
837	21	1.8	2329	20	AAQ73844	Human 7-transmembr	910	21	1.8	4040	20	AAQ34275	Human CDNA sequenc
838	21	1.8	2330	22	AAQ09285	Human TANGO 457 cD	911	21	1.8	4040	21	AAQ78573	Human lung tumour
839	21	1.8	2353	19	AAQ45981	A. thaliana sterol	912	21	1.8	4040	22	AAQ21456	Human ORF ORF3038
840	21	1.8	2371	21	AAQ18222	Lung cancer associ	913	21	1.8	4235	22	AAQ68399	Human ORF ORF2089
841	21	1.8	2371	22	AAQ63416	Human CD39-L2 spli	914	21	1.8	4668	21	AAQ77483	Mouse P4P6B1 OMA (
842	21	1.8	2376	20	AAQ72590	Human neurotropsin	c 915	21	1.8	4763	21	AAQ76534	Human CDNA sequenc
843	21	1.8	2383	21	AAQ18298	Lung cancer associ	916	21	1.8	4938	22	AAQ02457	Promoter of gene r
844	21	1.8	2384	20	AAQ36895	Human ABC-Transpor	917	21	1.8	5276	20	AAQ87397	Human IL-1ra BAC c
845	21	1.8	2401	22	AAQ56506	Arabidopsis CDC27A	c 918	21	1.8	5538	22	AAQ18660	Zucchini ACC synth
846	21	1.8	2434	22	AAQ56505	Arabidopsis CDC27A	c 919	21	1.8	5538	22	AAQ18660	Zucchini CP-ACC 1B
847	21	1.8	2466	22	AAQ32255	Human secreted pro	c 920	21	1.8	6298	22	AAQ75767	Zucchini ACC synth
848	21	1.8	2471	21	AAQ29050	Human prostate ser	c 921	21	1.8	6727	20	AAQ02993	Rupestria stem pit
849	21	1.8	2496	19	AAQ63189	Human CD39-L2 spli	c 922	21	1.8	7587	12	AAQ15133	Human ABC1 DNA seq
850	21	1.8	2497	22	AAQ63421	Human secreted pro	c 923	21	1.8	7587	19	AAQ15703	Western equine enc
851	21	1.8	2509	22	AAQ50146	Coding sequence fo	c 924	21	1.8	7587	22	AAQ04543	Human LMP-1 (HLMF-
852	21	1.8	2567	19	AAQ44889	Human p56-2 nucleo	c 925	21	1.8	7587	22	AAQ23620	Human glycosyl sul
853	21	1.8	2567	22	AAQ98602	Nucleotide sequenc	926	21	1.8	8743	20	AAQ99284	Human colorectal c
854	21	1.8	2570	22	AAQ87061	CDNA encoding a hu	927	21	1.8	9741	22	AAQ06120	Human low adenosin
855	21	1.8	2575	20	AAQ10654	CDNA encoding a hu	928	21	1.8	9854	22	AAQ35185	Human adenosine re
856	21	1.8	2584	20	AAQ10676	CDNA encoding a hu	c 929	21	1.8	11492	20	AAQ74107	Human low adenosin
857	21	1.8	2599	21	AAQ76501	Human ORF ORF2056	c 930	21	1.8	12470	21	AAQ87743	Human adenosine re
858	21	1.8	2610	21	AAQ23371	Human secreted pro	c 931	21	1.8	27150	22	AAQ02701	Human genomic sequ
c 859	21	1.8	2634	16	AAQ87841	Human neuronal cal	c 932	21	1.8	32204	22	AAQ15790	Nucleotide sequenc
c 860	21	1.8	2634	21	AAQ71722	Human calcium chan	c 933	21	1.8	32351	21	AAQ21307	Human chromosome 6
861	21	1.8	2654	20	AAQ88500	Human huplin/pi 13	c 934	21	1.8	32351	21	AAQ34791	Human adenosine re
862	21	1.8	2671	17	AAQ33648	Ras p21 interactin	c 935	21	1.8	40298	21	AAQ20913	Human ELAM-1 polyn
863	21	1.8	2671	20	AAQ09608	Human RGL CDNA. H	c 936	21	1.8	40298	21	AAQ21127	Human low adenosin
864	21	1.8	2672	21	AAQ16680	Human secreted pro	c 937	21	1.8	49312	21	AAQ51594	Human low adenosin
865	21	1.8	2693	22	AAQ63418	Human CD39-L2 spli	c 938	21	1.8	50000	21	AAQ64139	Human adenosine re
866	21	1.8	2700	22	AAQ33268	Human colon cancer	939	21	1.8	68940	20	AAQ57351	Human ELAM-1 polyn
c 867	21	1.8	2712	16	AAQ87836	Human neuronal cal	940	21	1.8	138169	21	AAQ34791	Human low adenosin
c 868	21	1.8	2712	21	AAQ71733	Human calcium chan	941	21	1.8	141589	21	AAQ21127	Human low adenosin
c 869	21	1.8	2754	21	AAQ49068	Arabidopsis thalia	942	21	1.8	141589	21	AAQ21152	Human low adenosin
870	21	1.8	2762	22	AAQ96066	Human ecto-phospha	943	21	1.8	141589	21	AAQ35005	Human adenosine re
871	21	1.8	2762	22	AAQ63386	Human CD39-L2 codi	944	21	1.8	141589	21	AAQ35030	Human adenosine re
872	21	1.8	2762	22	AAQ63422	Human CD39-L2 spli	945	21	1.8	141589	21	AAQ21442	Human ELAM-1 polyn
873	21	1.8	2789	21	AAQ93521	Human secreted pro	946	21	1.8	146981	21	AAQ21437	Human factor-relat
874	21	1.8	2805	22	AAQ63420	Human CD39-L2 spli	c 947	21	1.8	209273	21	AAQ21437	Arabidopsis thalia
875	21	1.8	2812	16	AAQ02327	Human fibroblast a	c 948	21	1.7	1082138	21	AAQ22305	Reverse transcript
876	21	1.8	2815	18	AAQ90148	Human fibroblast a	c 949	21	1.7	20	16	AAQ75564	LEC1 primer # 1.
877	21	1.8	2815	18	AAQ89286	Human fibroblast a	c 950	21	1.7	20	21	AAQ27451	LEC1 primer # 2.
878	21	1.8	2818	20	AAQ87710	Human Burkitt's ly	c 951	21	1.7	20	21	AAQ27452	LEC1 primer # 3.
879	21	1.8	2831	21	AAQ98739	Human serine prote	c 952	21	1.7	20	21	AAQ27453	LEC1 primer # 4.
880	21	1.8	2832	20	AAQ88499	Human huplin/pi 13	c 953	21	1.7	21	16	AAQ75629	Reverse transcript
881	21	1.8	2848	21	AAQ16656	Human secreted pro	c 954	21	1.7	21	16	AAQ75630	Reverse transcript
882	21	1.8	2863	22	AAQ85357	Murine SOCS-3 prom	c 955	21	1.7	21	16	AAQ75627	Reverse transcript
883	21	1.8	2868	19	AAQ55968	Human cytokine rec	c 956	21	1.7	21	31	AAQ81234	Rev-caspase-6 cDNA
884	21	1.8	2882	22	AAQ63424	Human CD39-L2 spli	c 957	21	1.7	31	20	AAQ96242	PCR primer used to
c 885	21	1.8	2952	21	AAQ99029	Human pancreatic c	c 958	21	1.7	35	22	AAQ63653	Plasmid pNC0-SB-H6
c 886	21	1.8	2970	16	AAQ87835	Human neuronal cal	c 959	21	1.7	36	22	AAQ23096	A. thaliana gene a
c 887	21	1.8	2970	21	AAQ71732	Human calcium chan	c 960	21	1.7	40	18	AAQ61446	Nucleotide anchore

FT /transl_except= (pos:579..581,aa:Xaa)
 FT /transl_except= (pos:585..587,aa:Xaa)
 FT /transl_except= (pos:594..596,aa:Xaa)
 FT /note= "Xaa-unknown; no stop codon"

XX WO200028058-A2.

PD 18-MAY-2000.

XX 09-NOV-1999; 99WO-US26514.

XX 09-NOV-1998; 98US-0107643.

PR 10-NOV-1998; 98US-0107810.

XX (PION-) PIONEER HI-BRED INT INC.

PA (DUPO) DU PONT DE NEMOURS & CO E I.

XX Lowe KS, Gordon-Kamm WJ, Klein TM, Rasco-Gaunt S, Cahoon RE;

PI Sun X, Hoerster GJ, Gregory CA, Nadimpalli R;

XX WPI; 2000-376568/32.

DR P-PSDB; AAY96219.

XX New HAP3-type CCAAT-box binding transcriptional activators,
 PT particularly leafy cotyledon 1 transcriptional activator, useful for
 PT inducing somatic embryogenesis or apomixis in a plant cell -

XX Claim 1; Page 86; 94pp; English.

CC The present sequence is the coding sequence of maize leafy cotyledon 1
 CC transcriptional activator, LEC1. This sequence encodes a HAP3-type
 CC CCAAT-box binding protein. LEC1 expression initiates the formation of
 CC embryo-like structures and improves growth and recovery of transformants.
 CC When apomixis occurs, i.e. the replacement of sexual reproduction by
 CC asexual reproduction, LEC1 expression in the nucellus integument, or
 CC cell specific expression in the megaspore mother cell would trigger
 CC embryo formation from maternal tissues only. This results in the
 CC production of seeds identical to the parent. Using LEC1, transgenic high
 CC yielding seeds could be developed. In addition, LEC1 could be used for
 CC positive selection of a transformed cell (transgenic plant), for
 CC increasing transformation efficiency and for increasing recovery of
 CC regenerated plants.

XX Sequence 622 BP; 131 A; 212 C; 164 G; 100 T; 15 other;

Query Match 3.3%; Score 39; DB 21; Length 622;
 Best Local Similarity 100.0%; Pred. No. 2.3e-05;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 373 tgtgggccatgagccgctcgcttcgacgactacgtcg 411
 |||||||||||||||||||||||||||||||||||||

Db 346 tgtgggccatgagccgctcgcttcgacgactacgtcg 384

RESULT 4

AAA27458

ID AAA27458 standard; cDNA; 763 BP.

XX AAA27458;

DT 11-SEP-2000 (first entry)

DE Maize LEC1 # 2 coding sequence.

XX Maize; leafy cotyledon 1 transcriptional activator; LEC1; apomixis;
 KW selectable marker; transgenic plant; transgenic seed; HAP3; ss.

XX Zea mays.

PH Key Location/Qualifiers

FT CDS 1..483

FT /*tag= a

FT /product= "Maize LEC1 # 2"
 FT /partial

PN WO200028058-A2.

PD 18-MAY-2000.

XX 09-NOV-1999; 99WO-US26514.

XX 09-NOV-1998; 98US-0107643.

PR 10-NOV-1998; 98US-0107810.

XX (PION-) PIONEER HI-BRED INT INC.

PA (DUPO) DU PONT DE NEMOURS & CO E I.

XX Lowe KS, Gordon-Kamm WJ, Klein TM, Rasco-Gaunt S, Cahoon RE;

PI Sun X, Hoerster GJ, Gregory CA, Nadimpalli R;

XX WPI; 2000-376568/32.

DR P-PSDB; AAY96218.

XX New HAP3-type CCAAT-box binding transcriptional activators,
 PT particularly leafy cotyledon 1 transcriptional activator, useful for
 PT inducing somatic embryogenesis or apomixis in a plant cell -

PS Claim 1; Page 84-85; 94pp; English.

XX The present sequence is the coding sequence of maize leafy cotyledon 1
 CC transcriptional activator, LEC1. This sequence encodes a HAP3-type
 CC CCAAT-box binding protein. LEC1 expression initiates the formation of
 CC embryo-like structures and improves growth and recovery of transformants.
 CC When apomixis occurs, i.e. the replacement of sexual reproduction by
 CC asexual reproduction, LEC1 expression in the nucellus integument, or
 CC cell specific expression in the megaspore mother cell would trigger
 CC embryo formation from maternal tissues only. This results in the
 CC production of seeds identical to the parent. Using LEC1, transgenic high
 CC yielding seeds could be developed. In addition, LEC1 could be used for
 CC positive selection of a transformed cell (transgenic plant), for
 CC increasing transformation efficiency and for increasing recovery of
 CC regenerated plants.

XX Sequence 763 BP; 131 A; 255 C; 241 G; 136 T; 0 other;

Query Match 3.3%; Score 39; DB 21; Length 763;
 Best Local Similarity 100.0%; Pred. No. 2.2e-05;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 373 tgtgggccatgagccgctcgcttcgacgactacgtcg 411
 |||||||||||||||||||||||||||||||||||||

Db 35 tgtgggccatgagccgctcgcttcgacgactacgtcg 73

RESULT 5

AAA27460

ID AAA27460 standard; cDNA; 1121 BP.

XX AAA27460;

DT 11-SEP-2000 (first entry)

DE Soybean LEC1 # 2 coding sequence.

XX Soybean; leafy cotyledon 1 transcriptional activator; LEC1; apomixis;
 KW selectable marker; transgenic plant; transgenic seed; HAP3; ss.

OS Glycine max.

PH Key Location/Qualifiers

FT CDS 3..1121

FT /*tag= a

FT /product= "Soybean LEC1 # 2"

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FT /transl_except= (pos:741..746,aa:Gln)
FT /transl_except= (pos:765..770,aa:Cys)
FT /transl_except= (pos:783..788,aa:Leu)
FT /transl_except= (pos:822..827,aa:Ser)
FT /transl_except= (pos:828..833,aa:Ser)
FT /transl_except= (pos:930..935,aa:Tyr)
FT /transl_except= (pos:945..950,aa:Ala)
FT /transl_except= (pos:999..1007,aa:Trp)
FT /transl_except= (pos:1008..1016,aa:Trp)
FT /transl_except= (pos:1059..1064,aa:Asn)
FT /transl_except= (pos:1095..1100,aa:Cys)
FT /transl_except= (pos:1103..1106,aa:Phe)
FT /note= "Codons have apparent insertions of three
FT nucleotides which encode stop codons"
XX
XX WO200028058-A2.
PN
XX
XX 18-MAY-2000.
PD
XX
XX 09-NOV-1999; 99WO-US26514.
PF
XX
XX 09-NOV-1998; 98US-0107643.
PR
XX
XX 10-NOV-1998; 98US-0107810.
PR
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX Lowe KS, Gordon-Kamm WJ, Klein TM, Rasco-Gaunt S, Cahoon RE;
XX Sun X, Hoerster GJ, Gregory CA, Nadimpalli R;
XX
XX WPI: 2000-376568/32.
DR
XX
XX P-PSDB; AAY96220, AAY96224.
DR
XX
XX New HAP3-type CCAAT-box binding transcriptional activators,
XX particularly leafy cotyledon 1 transcriptional activator, useful for
XX inducing somatic embryogenesis or apomixis in a plant cell -
XX
XX Claim 1: Page 87-89; 94pp; English.
XX
XX The present sequence is the coding sequence of soybean leafy cotyledon 1
XX transcriptional activator, LEC1. This sequence encodes a HAP3-type
XX CCAAT-box binding protein. LEC1 expression initiates the formation of
XX embryo-like structures and improves growth and recovery of transformants.
XX When apomixis occurs, i.e. the replacement of sexual reproduction by
XX asexual reproduction, LEC1 expression in the nucellus integument, or
XX cell specific expression in the megaspore mother cell would trigger
XX embryo formation from maternal tissues only. This results in the
XX production of seeds identical to the parent. Using LEC1, transgenic high
XX yielding seeds could be developed. In addition, LEC1 could be used for
XX positive selection of a transformed cell (transgenic plant), for
XX increasing transformation efficiency and for increasing recovery of
XX regenerated plants.
XX
XX Sequence 1121 BP; 324 A; 233 C; 263 G; 301 T; 0 other;
XX
XX Query Match 2.7%; Score 32; DB 21; Length 1121;
XX Best Local Similarity 100.0%; Pred. No. 0.0065;
XX Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 279 gagtcgtcgtcgagatcatcagttcatcac 310
XX ||||||||||||||||||||||||||||
XX Db 279 gagtcgtcgtcgagatcatcagttcatcac 310
XX
XX RESULT 6
XX AAA27461
XX ID AAA27461 standard; cDNA; 796 BP.
XX
XX AAA27461;
XX

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XX 11-SEP-2000 (first entry)
XX
XX Soybean LEC1 # 3 coding sequence.
XX
XX Soybean: leafy cotyledon 1 transcriptional activator; LEC1; apomixis;
XX selectable marker; transgenic plant; transgenic seed; HAP3; ss.
XX
XX Glycine max.
XX
XX Key Location/Qualifiers
XX CDS 1..516
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XX /product= "Soybean LEC1 # 3"
XX /partial
XX
XX WO200028058-A2.
XX
XX 18-MAY-2000.
PD
XX
XX 09-NOV-1999; 99WO-US26514.
PF
XX
XX 09-NOV-1998; 98US-0107643.
PR
XX
XX 10-NOV-1998; 98US-0107810.
PR
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX Lowe KS, Gordon-Kamm WJ, Klein TM, Rasco-Gaunt S, Cahoon RE;
XX Sun X, Hoerster GJ, Gregory CA, Nadimpalli R;
XX
XX WPI: 2000-376568/32.
DR
XX
XX P-PSDB; AAY96221.
DR
XX
XX New HAP3-type CCAAT-box binding transcriptional activators,
XX particularly leafy cotyledon 1 transcriptional activator, useful for
XX inducing somatic embryogenesis or apomixis in a plant cell -
XX
XX Claim 1: Page 90-91; 94pp; English.
XX
XX The present sequence is the coding sequence of soybean leafy cotyledon 1
XX transcriptional activator, LEC1. This sequence encodes a HAP3-type
XX CCAAT-box binding protein. LEC1 expression initiates the formation of
XX embryo-like structures and improves growth and recovery of transformants.
XX When apomixis occurs, i.e. the replacement of sexual reproduction by
XX asexual reproduction, LEC1 expression in the nucellus integument, or
XX cell specific expression in the megaspore mother cell would trigger
XX embryo formation from maternal tissues only. This results in the
XX production of seeds identical to the parent. Using LEC1, transgenic high
XX yielding seeds could be developed. In addition, LEC1 could be used for
XX positive selection of a transformed cell (transgenic plant), for
XX increasing transformation efficiency and for increasing recovery of
XX regenerated plants.
XX
XX Sequence 796 BP; 208 A; 174 C; 188 G; 226 T; 0 other;
XX
XX Query Match 2.2%; Score 26; DB 21; Length 796;
XX Best Local Similarity 100.0%; Pred. No. 0.99;
XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 264 aaggagacgacgagtcgagtcgctc 289
XX ||||||||||||||||||||||||
XX Db 112 aaggagacgacgagtcgagtcgctc 137
XX
XX RESULT 7
XX AAC93983
XX ID AAC93983 standard; cDNA; 417 BP.
XX
XX AAC93983;
XX
XX 19-FEB-2001 (first entry)
XX

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```

XX DE Cat flea hindgut and Malpighian tubule (HMT) cDNA, SEQ ID NO:478.
XX DE
XX KW Cat flea; hindgut and Malpighian tubule nucleic acid; HMT;
XX KW flea infestation; vaccine; antiparasitic; therapeutic target;
XX KW diagnosis; detection; ss.
XX OS Ctenocephalides felis.
XX PN WO200061621-A2.
XX PD 19-OCT-2000.
XX PF 07-APR-2000; 2000WO-US09437.
XX PR 09-APR-1999; 99US-0128704.
XX PA (HESK-) HESKA CORP.
XX PI Brandt KS, Gaines PJ, Stinchcomb DT, Wisniewski N;
XX DR WPI; 2000-656323/63.
XX PT Flea Malpighian tubule and head and nerve cord tissue derived nucleic
XX PT acids useful for the prevention, diagnosis and treatment of flea
XX PT infestations -
XX PS Claim 26; Page 403; 964pp; English.
XX CC The invention relates to novel cat flea (Ctenocephalides felis) nucleic
XX CC acids which are expressed in hindgut and Malpighian tubule (HMT) tissue
XX CC or head and nerve cord (HNC) tissue. The invention also relates to the
XX CC encoded proteins. The invention additionally encompasses expression
XX CC constructs, recombinant viruses and recombinant cells comprising the
XX CC nucleic acids of the invention, recombinant production of the proteins,
XX CC antibodies against the proteins, a method of identifying inhibitors of
XX CC the proteins, and compositions comprising the inhibitors for
XX CC administration to an animal. The nucleic acids, and the proteins they
XX CC encode may be used in the prevention, treatment and diagnosis of diseases
XX CC associated with flea infestations. For example, the nucleic acids may be
XX CC used to produce an HMT or HNC protein according to standard recombinant
XX CC DNA methodology by inserting the nucleic acids into a host cell and
XX CC culturing the cell to express the protein. The HMT and HNC nucleic acids
XX CC may also be used as DNA probes in diagnostic assays (e.g., PCR) to detect
XX CC and quantitate the presence of cat flea or other homologous nucleic acid
XX CC sequences in samples. They may also be used to study the expression and
XX CC function of the proteins and their role in metabolism. The HMT and HNC
XX CC proteins may be used as antigens in the production of specific
XX CC antibodies, and in assays to identify modulators (agonists and
XX CC antagonists) of HMT and/or HNC protein expression and activity. The
XX CC anti-HMT/HNC protein antibodies and antagonists may also be used to
XX CC downregulate protein expression and activity. The antibodies may also be
XX CC used as diagnostic agents for detecting the presence of flea polypeptides
XX CC in samples (e.g., by enzyme linked immunosorbent assay (ELISA)). The
XX CC present sequence represents a cat flea HMT cDNA of the invention.
XX SQ Sequence 417 BP; 172 A; 64 C; 63 G; 118 T; 0 other;

Query Match 2.1%; Score 25; DB 21; Length 417;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
| | | | | | | | | | | | | | | | | |
Db 391 ttatttcaaaaaaaaaaaaaaaaaa 415

RESULT 8
AAC94808
XX AAC94808 standard; cDNA; 417 BP.
XX ID
XX AC AAC94808;

```

```

XX DT 19-FEB-2001 (first entry)
XX DE
XX DE Cat flea hindgut and Malpighian tubule (HMT) cDNA, SEQ ID NO:1303.
XX KW Cat flea; hindgut and Malpighian tubule nucleic acid; HMT;
XX KW flea infestation; vaccine; antiparasitic; therapeutic target;
XX KW diagnosis; detection; ss.
XX OS Ctenocephalides felis.
XX PN WO200061621-A2.
XX PD 19-OCT-2000.
XX PF 07-APR-2000; 2000WO-US09437.
XX PR 09-APR-1999; 99US-0128704.
XX PA (HESK-) HESKA CORP.
XX PI Brandt KS, Gaines PJ, Stinchcomb DT, Wisniewski N;
XX DR WPI; 2000-656323/63.
XX PT Flea Malpighian tubule and head and nerve cord tissue derived nucleic
XX PT acids useful for the prevention, diagnosis and treatment of flea
XX PT infestations -
XX PS Claim 26; Page 665; 964pp; English.
XX CC The invention relates to novel cat flea (Ctenocephalides felis) nucleic
XX CC acids which are expressed in hindgut and Malpighian tubule (HMT) tissue
XX CC or head and nerve cord (HNC) tissue. The invention also relates to the
XX CC encoded proteins. The invention additionally encompasses expression
XX CC constructs, recombinant viruses and recombinant cells comprising the
XX CC nucleic acids of the invention, recombinant production of the proteins,
XX CC antibodies against the proteins, a method of identifying inhibitors of
XX CC the proteins, and compositions comprising the inhibitors for
XX CC administration to an animal. The nucleic acids, and the proteins they
XX CC encode may be used in the prevention, treatment and diagnosis of diseases
XX CC associated with flea infestations. For example, the nucleic acids may be
XX CC used to produce an HMT or HNC protein according to standard recombinant
XX CC DNA methodology by inserting the nucleic acids into a host cell and
XX CC culturing the cell to express the protein. The HMT and HNC nucleic acids
XX CC may also be used as DNA probes in diagnostic assays (e.g., PCR) to detect
XX CC and quantitate the presence of cat flea or other homologous nucleic acid
XX CC sequences in samples. They may also be used to study the expression and
XX CC function of the proteins and their role in metabolism. The HMT and HNC
XX CC proteins may be used as antigens in the production of specific
XX CC antibodies, and in assays to identify modulators (agonists and
XX CC antagonists) of HMT and/or HNC protein expression and activity. The
XX CC anti-HMT/HNC protein antibodies and antagonists may also be used to
XX CC downregulate protein expression and activity. The antibodies may also be
XX CC used as diagnostic agents for detecting the presence of flea polypeptides
XX CC in samples (e.g., by enzyme linked immunosorbent assay (ELISA)). The
XX CC present sequence represents a cat flea HMT cDNA of the invention.
XX SQ Sequence 417 BP; 172 A; 64 C; 63 G; 118 T; 0 other;

Query Match 2.1%; Score 25; DB 21; Length 417;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
| | | | | | | | | | | | | | | | | |
Db 391 ttatttcaaaaaaaaaaaaaaaaaa 415

RESULT 9
AAC94808
XX AAC94808 standard; cDNA; 1234 BP.
XX ID
XX AC AAC94808;

```

XX AAZ34964;
 XX AC
 XX DT
 XX 28-FEB-2000 (first entry)
 XX DE Soybean neutral triacylglycerol lipase cDNA.
 XX KW Triacylglycerol lipase; soybean; fatty acid; seed oil;
 XX KW vegetable oil; transgenic plant; ss.
 XX OS
 XX Oryza sativa.
 XX FH Key Location/Qualifiers
 XX CDS 173..913
 XX FT /*tag= a
 XX PN W0955883-A2.
 XX XX
 XX 04-NOV-1999.
 XX XX
 XX 29-APR-1999; 99WO-US09280.
 XX PF
 XX 30-APR-1998; 98US-0083688.
 XX PR
 XX XX
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 XX PA
 XX CAHOON EB, CAHOON RE, KINNEY AJ, RAFALSKI JA;
 XX PI
 XX WPI; 2000-062036/05.
 XX DR P-PSDB; AAY32315.
 XX DR
 XX Novel plant triacylglycerol lipase polynucleotides used to alter the
 XX level of the enzyme in transgenic plants -
 XX PT
 XX Claim 7; Page 58; 65pp; English.
 XX PS
 XX This is the nucleotide sequence of a contig assembled from the
 XX entire cDNA insert in clone ser.pk0058.b1 and a portion of the cDNA
 XX insert in clone sahlc.pk001.k20 encoding a substantial portion (see
 XX AAY32315) of a soybean neutral triacylglycerol lipase (TAGL). The
 XX clones were isolated from soybean root and Authority herbicide
 XX sprayed cDNA libraries. Novel acid and neutral TAGL polypeptides
 XX (see AAY32301-17) and polynucleotides (see AAZ34950-66) from corn,
 XX Catalpa, rice, soybean and wheat tissues are disclosed. The enzymes
 XX may be prepared recombinantly and used to raise antibodies, which
 XX are used for detecting the enzymes in situ in cells or in vitro in
 XX cell extracts. The polynucleotides may be used to create transgenic
 XX plants in which the TAGL levels are present at higher or lower levels
 XX than normal, or in cell types or developmental processes where they are
 XX not normally found. This would alter the level of triacylglycerol and
 XX cholesterol esters found in those cells. Accumulation of fatty acids
 XX with unusual structures may be a positive phenotype in plants used for
 XX foods. In addition, it may be desirable to eliminate expression of TAGL
 XX genes for certain applications. TAGL enzymes may also be useful for the
 XX processing of plant seed oils and for the development of novel seed
 XX oils. The TAGL enzymes can also be used as targets to facilitate the
 XX design and/or identification of inhibitors of those enzymes that may be
 XX useful as herbicides. This is desirable because inhibition of the
 XX activity of either of the enzymes could lead to an inhibition of plant
 XX growth. The polynucleotides also serve as a source of probes and
 XX primers, which are useful for genetic mapping, as markers for traits
 XX linked to those genes, and to isolate homologous sequences from other
 XX species.
 XX Sequence 1234 BP; 390 A; 196 C; 273 G; 375 T; 0 other;
 XX
 XX Query Match 2.1%; Score 25; DB 21; Length 1234;
 XX Best Local Similarity 100.0%; Pred. No. 2.1;
 XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
 XX ||||||||||||||||||||||||||||

Db 1187 ttatttcaaaaaaaaaaaaaaaaaa 1211
 RESULT 10
 AAN60472/c
 ID AAN60472 standard; DNA; 4590 BP.
 XX AC AAN60472;
 XX XX
 XX 24-AUG-1991 (first entry)
 XX DE Sequence encoding the ring-infected Erythrocyte Surface Antigen
 XX (RESA).
 XX KW Malaria vaccine; antigen; epitope; ss.
 XX OS Plasmodium falciparum.
 XX FH Key Location/Qualifiers
 XX exon 801..995
 XX FT /*tag= a
 XX FT 1199..4225
 XX FT /*tag= b
 XX PN W08601802-A.
 XX XX
 XX 27-MAR-1986.
 XX PD
 XX 11-SEP-1985; 85WO-0006960.
 XX PF
 XX 11-SEP-1984; 84AU-0007067.
 XX PR 11-SEP-1984; 84AU-0007066.
 XX PR 10-SEP-1985; 85AU-0047326.
 XX XX
 XX (HALL-) HALL INST MED RES.
 XX PA
 XX Kemp DJ, Anders R, Coppel RL, Brown G, Saint RB, Cowman AF;
 XX WPI; 1986-094065/14.
 XX DR P-PSDB; AAP60569.
 XX DR
 XX DNA coding for Plasmodium falciparum antigens - expressing
 XX poly:peptide(s) having antigenicity of RESA or FIRA antigens of P
 XX falciparum
 XX Claim 4; Fig 1; 55pp; English.
 XX PS The inventors claim a novel DNA molecule which comprises a
 XX nucleotide sequence corresp. to all or a portion of the base
 XX sequence coding RESA (AAN60472) or FIRA (AAN60473). RESA and FIRA have
 XX antigenicity suitable for providing protective immunity against
 XX Plasmodium falciparum malarial infections.
 XX Sequence 4590 BP; 1933 A; 437 C; 673 G; 1547 T; 0 other;
 XX
 XX Query Match 2.1%; Score 25; DB 7; Length 4590;
 XX Best Local Similarity 100.0%; Pred. No. 1.6;
 XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
 XX ||||||||||||||||||||||||||||
 XX Db 1030 TTATTTCAAAAAAAAAAAAAAAAAA 1006
 RESULT 11
 AAZ90034/c
 ID AAZ90034 standard; DNA; 36 BP.
 XX AC AAZ90034;
 XX XX
 XX 08-MAY-2000 (first entry)
 XX DT
 XX XX

DE Reverse PCR primer used to amplify delta E2.
 XX Hepatitis C virus; envelope protein E2; hypervariable region 1;
 KW peptide library; treatment; prevent infection; antibody production;
 KW PCR primer; ss.
 XX
 OS Hepatitis C virus.
 XX
 PN WO9960132-A1.
 XX
 PD 25-NOV-1999.
 XX
 XX 14-MAY-1999; 99WO-EP03344.
 XX
 XX 19-MAY-1998; 98GB-0010756.
 XX
 PA (RICE-) IST RICERCHIE BIOL MOLECOLARE ANGELETTI.
 XX
 PI Nicosia A, Lahm A, Tramontano A, Cortese R;
 XX
 XX WPI; 2000-126382/11.
 XX
 PT A new peptide library from hepatitis C virus, useful for production of
 PT treatment for hepatitis C -
 XX
 XX Example 6; Page 80; 126pp; English.
 XX
 PS This sequence represents a PCR primer used to amplify delta E2, the gene
 CC encoding an envelope protein of Hepatitis C virus. The PCR product is
 CC used in the construction of the peptide library of the invention. The
 CC invention relates to a library of peptides which have an immunologically
 CC reactive epitope of the hypervariable region 1 (HVR1) of envelope
 CC protein 2 (E2) of hepatitis C virus. The peptides correspond to formulae
 CC given in the specification (see AAV78596-Y78598). The peptides can be
 CC used in a method to select antibodies which react with the HVR1 of E2 of
 CC hepatitis C virus, through the selection of those antibodies which bind
 CC to the peptides. The peptides from hepatitis C virus hypervariable region
 CC 1 of the envelope protein E2 are used to produce a medicament for raising
 CC or increasing levels of antibodies able to bind HCV (hepatitis C virus)
 CC HVR1 epitopes in a mammal. The medicament is used to treat or prevent an
 CC HCV infection.
 XX
 SQ Sequence 36 BP; 3 A; 5 C; 17 G; 11 T; 0 other;

Query Match 2.0%; Score 24; DB 21; Length 36;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 579 ctaccgcaccaccaccaccaccac 602
 ||||||||||||||||||||
 Db 36 CTACCGCACCACCACCACCACCAC 13

RESULT 12
 AAV73459
 ID AAV73459 standard; cDNA; 500 BP.
 XX
 AC AAV73459;
 XX
 DT 26-APR-1999 (first entry)
 XX
 DE Flea saliva protein nucleic acid nfspL3-500.
 XX
 KW Flea saliva protein; nfspL3-500; allergic dermatitis; allergen;
 KW allergy; therapy; diagnosis; vaccine; ectoparasite; ss.
 XX
 OS Ctenocephalides sp.
 XX
 XX KEY Location/Qualifiers
 FH 1..186
 FT CDS /*tag= a
 FT
 XX

PN WO9845408-A2.
 XX
 PD 15-OCT-1998.
 XX
 PF 15-OCT-1997; 97WO-US18669.
 XX
 PR 10-APR-1997; 97WO-US05959.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI Weber ER;
 XX
 DR WPI; 1998-594480/50.
 DR P-PSDB; AAW82393.
 XX
 XX New isolated ectoparasite saliva genes - used to develop products
 PT for the diagnosis, prevention, treatment and determining
 PT susceptibility to allergic dermatitis
 XX
 PS Claim 1; Page 157; 172pp; English.
 XX
 CC This is the nucleotide sequence of nfspL3-500, which encodes a
 CC non-full-length flea salivary protein, termed pfspL3-61 (see
 CC AAW82393). The clone was obtained by PCR amplification (see
 CC AAV73455-58) from a whole flea cDNA library. Its sequence shows no
 CC significant homology to known sequences. A DNA probe based on
 CC nfspM(N)80 may be useful for isolating the full-length clone.
 CC The invention is directed to methods for isolating ectoparasite
 CC saliva proteins (ESPs), including flea saliva proteins. It
 CC provides ESps (claimed, see AAW82382-93), nucleic acid molecules
 CC encoding them, methods for their recombinant production,
 CC therapeutic compositions for treating allergic dermatitis that
 CC comprise at least one ESP, as well as assay kits for testing if an
 CC animal has, or is susceptible to, allergic dermatitis, and a method
 CC of desensitising a host animal to allergic dermatitis using ESps.
 CC The ESps can also be used for the production of antibodies useful
 CC in diagnosis or in vaccines for passive immunisation against
 CC allergic dermatitis.
 XX
 SQ Sequence 500 BP; 230 A; 62 C; 58 G; 150 T; 0 other;

Query Match 2.0%; Score 24; DB 19; Length 500;
 Best Local Similarity 100.0%; Pred. No. 5.7;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attattcacaacacacacacacac 1171
 ||||||||||||||||||||
 Db 477 attattcacaacacacacacacac 500

RESULT 13
 AAV73460/C
 ID AAV73460 standard; cDNA; 500 BP.
 XX
 AC AAV73460;
 XX
 DT 26-APR-1999 (first entry)
 XX
 DE Flea saliva protein nucleic acid nfspL3-500 (complement).
 XX
 KW Flea saliva protein; nfspL3-500; allergic dermatitis; allergen;
 KW allergy; therapy; diagnosis; vaccine; ectoparasite; ss.
 XX
 OS Ctenocephalides sp.
 XX
 PN WO9845408-A2.
 XX
 PD 15-OCT-1998.
 XX
 PF 15-OCT-1997; 97WO-US18669.
 XX
 PR 10-APR-1997; 97WO-US05959.


```

XX PA (HESK-) HESKA CORP.
XX PI Weber ER;
XX XX
XX DR WPI; 1998-594480/50.
XX PT
XX PT New isolated ectoparasite saliva genes - used to develop products
XX PT for the diagnosis, prevention, treatment and determining
XX PT susceptibility to allergic dermatitis
XX PS Claim 1; Page 158; 172pp; English.
XX CC
XX CC This is the nucleotide sequence of nucleic acid nfpL3-500
XX CC complementary strand. The coding strand (see AAV73459) encodes a
XX CC non-full-length flea salivary protein, termed PfspL3-61 (see
XX CC AW82293). The clone was obtained by PCR amplification (see
XX CC AAV73455-58) from a whole flea cDNA library. Its sequence shows no
XX CC significant homology to known sequences. A DNA probe based on
XX CC nfpM(N)880 may be useful for isolating the full-length clone.
XX CC The invention is directed to methods for isolating ectoparasite
XX CC saliva proteins (ESPs), including flea saliva proteins. It
XX CC provides ESs (claimed, see AAW82382-93), nucleic acid molecules
XX CC encoding them, methods for their recombinant production,
XX CC therapeutic compositions for treating allergic dermatitis that
XX CC comprise at least one ESP, as well as assay kits for testing if an
XX CC animal has, or is susceptible to, allergic dermatitis, and a method
XX CC of desensitising a host animal to allergic dermatitis using ESs.
XX CC The ESs can also be used for the production of antibodies useful
XX CC in diagnosis or in vaccines for passive immunisation against
XX CC allergic dermatitis.
XX SQ Sequence 500 BP; 150 A; 58 C; 62 G; 230 T; 0 other;

Query Match 2.0%; Score 24; DB 19; Length 500;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attattcaaaaaaaaaaaaaa 1171
DB 24 ATTATTTCAAAAAAAAAAAAAA 1

RESULT 14
AAH87686/C
ID AAH87686 standard; cDNA; 653 BP.
XX AC AAH87686;
XX DT
XX DT 25-SEP-2001 (first entry)
XX DE
XX DE Peppermint plant oil gland expressed cDNA 42.
XX KW Peppermint; plant oil gland cell; terpenoid essential oil; resin;
XX KW genetic mapping; antisense suppression; recombinant expression; ss.
XX OS Mentha x piperita.
XX XX
XX XX WO200153319-A1.
XX PN
XX PD 26-JUL-2001.
XX XX
XX XX 19-JAN-2001; 2001WO-US02567.
XX XX
XX XX 20-JAN-2000; 2000US-0177264.
XX PA (CROT/) CROTEAU R B.
XX PA (LANG/) LANGE B M.
XX PA (WILD/) WILDUNG M R.
XX PI Croteau RB, Lange BM, Wildung MR;
XX XX

XX DR WPI; 2001-488706/53.
XX XX
XX PT New nucleic acid molecules corresponding to mRNA molecules expressed in
XX PT peppermint oil glands for enhancing expression of plant oil gland cell
XX PT proteins -
XX PS Claim 1; Page 93; 251pp; English.
XX CC
XX CC The invention relates to nucleic acid molecules (AAH87645-AAH88116) that
XX CC correspond to all or part of a mRNA molecule expressed in plant oil
XX CC gland cells, especially peppermint and plant oil glands that produce
XX CC terpenoid essential oils and resins. The nucleic acids are useful for
XX CC genetically mapping a plant genome for genes expressed in plant oil
XX CC gland cells and to suppress (for example by antisense suppression) or
XX CC enhance their expression (for example by genetically transforming a
XX CC plant cell with a replicable expression vector that expresses one or more
XX CC proteins naturally expressed in plant oil gland cells). The nucleic acids
XX CC are also useful for recombinant expression of plant oil gland proteins
XX CC required for terpenoid essential oil and/or resin production in bacterial
XX CC and/or yeast cells.
XX SQ Sequence 653 BP; 165 A; 150 C; 134 G; 202 T; 2 other;

Query Match 2.0%; Score 24; DB 22; Length 653;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1150 tatttcaaaaaaaaaaaaaa 1173
DB 28 TATTTCAAAAAAAAAAAAAA 5

RESULT 15
AAA59457
ID AAA59457 standard; DNA; 886 BP.
XX AC AAA59457;
XX DT
XX DT 14-NOV-2000 (first entry)
XX DE
XX DE Nucleotide sequence of a soybean type I glutathione-S-transferase.
XX KW Soybean; glutathione-S-transferase; GST; detoxification;
XX KW xenobiotic compound; herbicide-tolerance; transgenic plant;
XX KW herbicide synergist; ss.
XX OS Glycine max.
XX XX
XX FH Key Location/Qualifiers
XX FT CDS 18..623
XX FT /*tag= a
XX FT /product= "glutathione-S-transferase"
XX XX
XX PN WO200047728-A2.
XX PD
XX PD 17-AUG-2000.
XX PF 10-FEB-2000; 2000WO-US03347.
XX XX
XX PR 10-FEB-1999; 99US-0247373.
XX XX
XX XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX PA
XX PI McGonigle B, O'Keefe DP;
XX XX
XX XX WPI; 2000-549144/50.
XX DR P-PSDB; AAB07826.
XX XX
XX PT Soybean glutathione-S-transferase polypeptides and polynucleotides used
XX PT to produce herbicide tolerant transgenic plants and to screen for
XX PT inhibitors or substrates of the enzyme -
XX XX

```

PS Claim 2; Page 55; 84pp; English.

XX The present sequence encodes a soybean glutathione-S-transferase
CC (GST) enzyme. The enzyme is involved in the detoxification of
CC xenobiotic compounds in plants and seeds. The GST polynucleotides
CC and polypeptides are used for the production of herbicide-tolerant
CC transgenic plants, and for the development of screening assays to
CC identify GST inhibitors and substrates, which can be used as
CC herbicide synergists. GST gene specific probes can be used in gene
CC identification methods. The recombinant GST enzymes can be used to
CC produce enzyme specific antibodies which are used to detect the
CC enzymes in situ in cells or in vitro in cell extracts.

XX SQ Sequence 886 BP; 250 A; 166 C; 199 G; 271 T; 0 other;

Query Match 2.0%; Score 24; DB 21; Length 886;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1150 tatttcaaaaaaaaaaaaaa 1173
|||||
Db 863 tatttcaaaaaaaaaaaaaa 886

RESULT 16

AAZ53393
ID AA53393 standard; cDNA; 886 BP.

XX AC AA53393;

XX DT 04-OCT-2000 (first entry)

XX DE Clone se.127b04 nucleotide sequence encoding GST type I.

XX KW Soybean; glutathione-S-transferase; GST; detoxify; herbicide; stress;
XX KW transgenic plant; tolerant; plant breeding; ss.

XX OS Glycine max.

XX PN US6063570-A.

XX PD 16-MAY-2000.

XX PF 05-SEP-1997; 97US-0924747.

XX PR 05-SEP-1997; 97US-0924747.

XX PA (DUPO) DU PONT DE NEMOURS & CO E I.

XX PI McGonigle B, O'Keefe DP;

XX WPI: 2000-375487/32.

XX DR P-PSDB; AAB03731.

XX New Glutathione-S-Transferase enzymes and isolated nucleic acid
PT fragments encoding them, useful for detoxifying xenobiotic compounds in
PT plants and seeds, as well as in producing transgenic plants that are
PT herbicide-resistant

XX Claim 2; Column 25-26; 36pp; English.

XX This sequence was isolated from a soybean clone, and encodes a
CC Glutathione-S-Transferase (GST). The invention relates to isolated
CC nucleic acid fragments (see AA53393-A53406) which encode soybean GST
CC polypeptides (AAB03731-B03744). GSTs are a family of enzymes which
CC catalyze the conjugation of glutathione, homogluthathione and other
CC glutathione-like analogues, to a large range of hydrophobic,
CC electrophilic compounds. GSTs have been implicated in the detoxification
CC of certain herbicides. The GST nucleotide sequences are useful in the
CC construction of herbicide-tolerant transgenic plants, plants that are
CC tolerant to a wide variety of stresses, or plants in which the GST
CC enzymes are present at higher or lower levels than they are normally.

CC The nucleic acid fragments are also useful as probes for genetically and
CC physically mapping the genes that they are part of, and as markers for
CC traits linked to expression of the enzymes. This will be useful in plant
CC breeding in order to develop lines with desired phenotypes or in the
CC identification of mutants. The soybean GST enzymes are used to detoxify
CC xenobiotic compounds in plants and seeds. The enzymes are also useful as
CC targets to facilitate design and/or identify inhibitors of the enzymes
CC that may be used as herbicides or herbicide synergists. The GST enzymes
CC produced in the host cells, particularly in microbial host cells, are
CC useful in preparing antibodies to the enzymes. These antibodies are
CC useful for detecting the enzymes in situ in cells or in vitro in cell
CC extracts.

XX SQ Sequence 886 BP; 250 A; 166 C; 199 G; 271 T; 0 other;

Query Match 2.0%; Score 24; DB 21; Length 886;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1150 tatttcaaaaaaaaaaaaaa 1173
|||||
Db 863 tatttcaaaaaaaaaaaaaa 886

RESULT 17

AAZ94949

ID AA294949 standard; cDNA; 886 BP.

XX AC AA294949;

XX DT 01-AUG-2000 (first entry)

XX DE Soybean glutathione-S-transferase cDNA clone sel.27B04.

XX KW Soybean; glutathione-S-transferase; GST; xenobiotic;
XX KW detoxification; transgenic plant; herbicide tolerance; ss.

XX OS Glycine max.

XX FH Key Location/Qualifiers
XX CDS 18..623
XX FT /*tag= a
XX FT /EC_number= 2.5.1.18

XX PN WO200018936-A1.

XX PD 06-APR-2000.

XX PF 30-SEP-1998; 98WO-US20501.

XX PR 30-SEP-1998; 98WO-US20501.

XX PA (DUPO) DU PONT DE NEMOURS & CO E I.

XX PI McGonigle B, O'Keefe DP;

XX WPI: 2000-317517/27.

XX DR P-PSDB; AAY79512.

XX Nucleic acids encoding soybean glutathione-S-transferase enzymes useful
PT for conferring herbicide resistance to plants -

XX Claim 2; Page 39; 76pp; English.

XX The present sequence is that of the cDNA insert in clone
CC sel.27B04 encoding soybean class I glutathione-S-transferase
CC (GST, see AAY79512). The clone was isolated from a cDNA library
CC prepared from soybean embryo. The invention provides soybean GST
CC enzymes (see AAY79512-25) involved in the detoxification of
CC xenobiotic compounds, especially herbicides, in plants and seeds.
CC Chimeric genes encoding all or a portion of soybean GST enzymes,
CC host cells, and methods of recombinant production of soybean GST

CC enzymes are provided. The sequences are useful in the construction
 CC of herbicide-tolerant transgenic plants, in the recombinant
 CC production of GST enzymes, in the development of screening assays
 CC to identify compounds inhibitory to the GST enzymes (useful as
 CC herbicides or herbicide synergists), and in screening assays to
 CC identify chemical substrates of the GSTs.

SQ Sequence 886 BP; 250 A; 166 C; 199 G; 271 T; 0 other;

Query Match 2.0%; Score 24; DB 21; Length 886;
 Best Local Similarity 100.0%; Pred. No. 5.1;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1150 tatttcaaaaaaaaaaaaaaaaaa 1173

Db 863 tatttcaaaaaaaaaaaaaaaaaa 886

RESULT 18

AAF31572

ID AAF31572 standard; DNA; 886 BP.

XX AC AAF31572;

DT 09-APR-2001 (first entry)

DE Soybean type I GST cDNA.

XX Soybean; glutathione-S-transferase; herbicide; GST; ds.

XX Glycine max.

XX US6171839-B1.

XX 09-JAN-2001.

XX 22-APR-1999; 99US-0296715.

XX 05-SEP-1997; 97US-0924747.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX McGonigle B, O'Keefe DP;

XX WPI; 2001-136874/14.

XX Novel soybean glutathione-S-transferase enzymes useful as targets to
 PT facilitate design and/or identification of inhibitors of the enzyme,
 PT that are used as herbicides or herbicide synergists -

XX Claim 2; Column 25-26; 37pp; English.

CC The present invention relates to soybean glutathione-S-transferase
 CC proteins. The novel sequences are useful in the construction of
 CC herbicide tolerant transgenic plants, in the recombinant production
 CC of glutathione-S-transferase (GST) enzymes, in the development of
 CC screening assays to identify compounds inhibitory to the GST enzymes,
 CC and in screening assays to identify chemical substrates of the GSTs.

SQ Sequence 886 BP; 250 A; 166 C; 199 G; 271 T; 0 other;

Query Match 2.0%; Score 24; DB 22; Length 886;
 Best Local Similarity 100.0%; Pred. No. 5.1;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1150 tatttcaaaaaaaaaaaaaaaaaa 1173

Db 863 tatttcaaaaaaaaaaaaaaaaaa 886

RESULT 19

AAZ52292

ID AAZ52292 standard; cDNA; 1231 BP.

XX AC AAZ52292;

DT 18-JUL-2000 (first entry)

DE Maize replication protein A middle subunit homologue-7 (ZmRPAMSH7) cDNA.

XX Maize; Replication protein A; RPA; middle subunit; ZmRPAMSH; virucide;
 KW fungicide; insecticide; chromosome 5; DNA-binding protein; DNA repair;
 KW DNA metabolism; DNA replication; cell cycle; homologous recombination;
 KW pathogen resistance; fungi; virus; nematode; insect; gene therapy;
 KW genetic manipulation; ss.

OS Zea mays.

XX Key Location/Qualifiers

XX CDS 85..514

XX /tag= a

XX /product= "Maize replication protein A middle subunit

XX homologue-7"

XX /note= "Mapped to chromosome 5"

XX WO200015816-A2.

XX 23-MAR-2000.

XX 15-SEP-1999; 99WO-US21277.

XX 17-SEP-1998; 98US-0100690.

XX 11-MAR-1999; 99US-0123896.

XX (PION-) PIONEER HI-BRED INT INC.

XX Mahajan P;

XX WPI; 2000-271452/23.

XX P-PSDB; AAY70710.

XX New maize replication protein A useful for genetic transformation, gene
 PT targeting in plants and modulating DNA metabolism -

XX Claim 2c; Page 98-100; 101pp; English.

XX The present sequence is a cDNA encoding the maize replication protein A
 CC (RPA) middle subunit homologue-7 (ZmRPAMSH7). RPA is a single-stranded
 CC DNA-binding protein required for multiple processes in DNA metabolism,
 CC like DNA replication, repair mechanism (e.g. nucleotide excision and
 CC double stranded (ds) DNA break repair) and recombination. The gene
 CC for the ZmRPAMSH homologue is mapped to chromosome 5. This sequence
 CC has fungicide, virucide and insecticidal activity. DNA encoding RPA is
 CC used for modulating DNA metabolism, influencing cell cycle, enhancing
 CC homologous recombination and increasing pathogen resistance in plants.
 CC Pests that can be controlled include fungal pathogens, viruses,
 CC nematodes and insects. Antisense sequences can be used to block RPA
 CC expression and promote non-specific recombination events. RPA protein
 CC can be used to improve genetic manipulation and also in gene therapy.

XX Sequence 1231 BP; 338 A; 296 C; 303 G; 294 T; 0 other;

Query Match 2.0%; Score 24; DB 21; Length 1231;
 Best Local Similarity 100.0%; Pred. No. 4.8;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1150 tatttcaaaaaaaaaaaaaaaaaa 1173

Db 1196 tatttcaaaaaaaaaaaaaaaaaa 1219

RESULT 20

AAZ55043

ID AAF5043 standard; DNA; 1316 BP.
 AC AAF5043;
 XX
 DT 15-MAY-2001 (first entry)
 XX
 DE Nucleotide sequence of a calcium channel transport polypeptide.
 XX
 KW Calcium channel transport polypeptide; calcium trafficking;
 XX neural disorder; HIV-induced dementia; immune system disorder;
 KW rheumatoid arthritis; muscular disorder; muscle contractile dysfunction;
 KW reproductive disorder; gastrointestinal disorder; pulmonary disorder;
 KW cardiovascular disorder; arrhythmia; renal disorder;
 KW proliferative disorder; cancer; lung carcinoma; breast cancer; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 36..341
 FT CDS /*tag= a
 FT /product= "calcium channel transport polypeptide"
 XX
 PN WO200108635-A2.
 XX
 PD 08-FEB-2001.
 XX
 PE 27-JUL-2000; 2000WO-US20392.
 XX
 PR 28-JUL-1999; 99US-0145958.
 PR 18-AUG-1999; 99US-0149446.
 PR 14-MAR-2000; 2000US-0189064.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Ni J, Shi Y;
 XX
 DR WPI: 2001-138604/14.
 DR P-PSDB; AAB67466.
 XX
 PT New isolated nucleic acid useful for diagnosing, detecting, or treating
 PT or preventing diseases associated with anomalies in calcium trafficking
 PT across the plasma membrane -
 XX
 PS Claim 1; Page 254; 259pp; English.
 XX
 CC The present sequence encodes a calcium channel transport polypeptide.
 CC The polynucleotides, polypeptides, and antibodies are useful for
 CC preventing, treating, or ameliorating diseases associated with anomalies
 CC in calcium trafficking across the plasma membrane. They are used to
 CC diagnose, detect and treat or prevent diseases or conditions such as
 CC neural disorders (e.g. HIV-induced dementia), immune system disorders
 CC (e.g. rheumatoid arthritis), muscular disorders (e.g. muscle contractile
 CC dysfunction), reproductive disorders, gastrointestinal disorders, renal
 CC pulmonary disorders, cardiovascular disorders (e.g. arrhythmias), renal
 CC disorders, proliferative disorders, and/or cancerous diseases and
 CC conditions (e.g. lung carcinoma or breast cancer).
 XX
 SQ Sequence 1316 BP; 458 A; 227 C; 237 G; 394 T; 0 other;
 Query Match 2.0%; Score 24; DB 22; Length 1316;
 Best Local Similarity 100.0%; Pred. No. 4.7;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1150 tatttcaaaaaaaaaaaaaaaaaa 1173
 Db 1291 tatttcaaaaaaaaaaaaaaaaaa 1314
 RESULT 21
 AAH24830
 ID AAH24830 standard; DNA; 1372 BP.
 XX

AC AAH24830;
 XX
 DT 22-AUG-2001 (first entry)
 XX
 DE Nucleotide sequence of sense strand of cuticlin gene.
 XX
 KW Cuticlin; gene therapy; vaccine; helminth parasite; ss.
 XX
 OS Dirofilaria immitis.
 XX
 FH Key Location/Qualifiers
 FT CDS 392..1207
 FT /*tag= a
 FT /product= "cuticlin"
 XX
 PN US6248329-B1.
 XX
 PD 19-JUN-2001.
 XX
 PE 01-JUN-1999; 99US-0323427.
 XX
 PR 01-JUN-1998; 98US-0087435.
 XX
 PA (CHAN/) CHANDRASHEKAR R.
 PA (MORA/) MORALES T H.
 XX
 PI Chandrashekar R, Morales TH;
 XX
 DR WPI: 2001-396953/42.
 DR P-PSDB; AAB84259.
 XX
 PT Novel nucleic acid molecule encoding a Dirofilaria immitis cuticlin
 PT protein is useful as a vaccine to prevent parasitic helminth infection
 PT -
 XX
 PS Example 1; Column 43-44; 29pp; English.
 XX
 CC The specification describes a Dirofilaria immitis nucleic acid molecule,
 CC that encodes a cuticlin protein. The Dirofilaria immitis nucleic acid
 CC molecule is useful as a probe to identify nucleic acid molecules, as a
 CC primer to produce nucleic acids, as a therapeutic reagent, e.g., gene
 CC therapy to inhibit cuticlin activity or production, or in a vaccine to
 CC prevent infection with helminth parasites. The cuticlin protein,
 CC all be used in compositions to protect animals, especially mammals such
 CC as cats, dogs, and humans. The antibodies may be used to passively
 CC immunize an animal, or as reagents in assay to detect infection of
 CC helminths, or as tools to screen expression libraries to recover desired
 CC proteins. They may also be used to target cytotoxic agents to the
 CC parasite and kill it directly. The present sequence encodes a cuticlin
 CC polypeptide.
 XX
 SQ Sequence 1372 BP; 456 A; 229 C; 281 G; 406 T; 0 other;
 Query Match 2.0%; Score 24; DB 22; Length 1372;
 Best Local Similarity 100.0%; Pred. No. 4.7;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1150 tatttcaaaaaaaaaaaaaaaaaa 1173
 Db 1341 tatttcaaaaaaaaaaaaaaaaaa 1364
 RESULT 22
 AAH24831/c
 ID AAH24831 standard; DNA; 1372 BP.
 XX
 AC AAH24831;
 XX
 DT 22-AUG-2001 (first entry)
 XX
 DE Nucleotide sequence of antisense strand of cuticlin gene.

XX Cuticlin; gene therapy; vaccine; helminth parasite; ss.
 KW
 XX

OS Dirofilaria immitis.
 XX

XX US6248329-B1.
 XX

XX 19-JUN-2001.
 XX

XX 01-JUN-1999; 9905-0323427.
 XX

XX 01-JUN-1998; 9805-0087435.
 XX

XX (CHAN/) CHANDRASHEKAR R.
 XX

XX (MORA/) MORALES T H.
 XX

XX Chandrashekar R, Morales TH;
 XX

XX WPI; 2001-396953/42.
 XX

XX Novel nucleic acid molecule encoding a Dirofilaria immitis cuticlin
 PT protein is useful as a vaccine to prevent parasitic helminth infection
 PT

XX Example 1; Column 43-46; 29pp; English.
 XX

XX The specification describes a Dirofilaria immitis nucleic acid molecule,
 CC that encodes a cuticlin protein. The Dirofilaria immitis nucleic acid
 CC molecule is useful as a probe to identify nucleic acid molecules, as a
 CC primer to produce nucleic acids, as a therapeutic reagent, e.g., gene
 CC therapy to inhibit cuticlin activity or production, or in a vaccine to
 CC prevent infection with helminth parasites. The cuticlin protein,
 CC antibodies raised against it, and inhibitory compounds of cuticlin may
 CC all be used in compositions to protect animals, especially mammals such
 CC as cats, dogs, and humans. The antibodies may be used to passively
 CC immunize an animal, or as reagents in assay to detect infection of
 CC helminths, or as tools to screen expression libraries to recover desired
 CC proteins. They may also be used to target cytotoxic agents to the
 CC parasite and kill it directly. The present sequence represents the
 CC complement of DNA encoding a cuticlin polypeptide.
 XX

XX Sequence 1372 BP; 406 A; 281 C; 229 G; 456 T; 0 other;
 SQ

Query Match 2.0%; Score 24; DB 22; Length 1372;
 Best Local Similarity 100.0%; Pred. No. 4.7;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1150 tatttcaaaaaaiaaaaaaaaaa 1173
 |||||||||||||||||||||

DB 32 TATTTCAAAAAIAAAAAAAAAA 9

RESULT 23

AAAF16022

ID AA16022 standard; cDNA; 1399 BP.

XX AA16022;

XX 13-MAR-2001 (first entry)

DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:457.
 XX

KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
 KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
 KW vulnary; gastrointestinal; nephrotoxic; antineoplastic; gynaecological;
 KW antibacterial; gene therapy; immune; reproductive; renal;
 KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
 KW wound; infectious disease; ss.
 XX

OS Homo sapiens.
 XX

XX WO200055174-A1.
 XX

XX 21-SEP-2000.
 PD

XX 08-MAR-2000; 2000WO-US05988.
 XX

XX 12-MAR-1999; 9905-0124270.
 XX

XX (HUMA-) HUMAN GENOME SCI INC.
 PA (ROSE/) ROSEN C A.
 XX

XX Rosen CA, Ruben SM;
 PI

XX WPI; 2000-587513/55.
 XX

XX P-PSDB; AAB56819.
 DR

XX Prostate cancer associated gene sequences, referred to as prostate
 PT cancer antigens, useful for treatment, prevention, and diagnosis of
 PT disorders such as prostate cancer -
 XX

XX Claim 1; Page 934; 2338pp; English.
 PS

XX AA15566 to AA16505 encode the human prostate cancer associated
 CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
 CC The prostate cancer antigens can have neuroprotective, cytostatic,
 CC cardioactive, immunomodulatory, muscular, vulnary, gastrointestinal,
 CC nephrotoxic, antineoplastic, gynaecological and antibacterial activities,
 CC and can be used in gene therapy. The prostate cancer antigen
 CC polynucleotides may be used for detection of prostate cancer, chromosome
 CC identification, as chromosome markers, and for numerous other diagnostic
 CC or research purposes. The prostate cancer antigens may be used to treat
 CC disorders such as neural, immune, muscular, reproductive,
 CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
 CC disorders, wounds, and infectious diseases. AA16506 to AA16514 to
 CC AA57303 represent sequences used in the exemplification of the present
 CC invention.
 XX

SQ Sequence 1399 BP; 302 A; 402 C; 389 G; 303 T; 3 other;

Query Match 2.0%; Score 24; DB 21; Length 1399;
 Best Local Similarity 100.0%; Pred. No. 4.6;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1150 tatttcaaaaaaiaaaaaaaaa 1173
 |||||||||||||||||||||

DB 1344 tatttcaaaaaaiaaaaaaaaa 1367

RESULT 24

AAZ25133

ID AA225133 standard; cDNA; 1466 BP.

XX AA225133;
 AC

XX 13-DEC-1999 (first entry)
 DT

DE Human hypoxia induced gene HIG2 cDNA sequence.
 XX

XX Hypoxia induced gene; HIG; cancer; ischaemia; diagnosis; reperfusion;
 KW retinopathy; neonatal distress; pre-eclampsia; cardiac arrest; stroke;
 KW stress; hypoxia; ionising radiation; hypothermia; heat shock; ss.
 XX

OS Homo sapiens.
 XX

XX Key Location/Qualifiers
 XX CDS 274..465
 XX /*tag= a
 XX /product= "HIG2"

XX WO9948916-A2.
 XX

XX 30-SEP-1999.
 XX

PF 29-MAR-1999; 99WO-US06860.
XX
PR 27-MAR-1998; 98US-0049719.
XX
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (STRI) SRI INT.
XX
PI Denko NC, Giaccia AJ, Green CJ, Laderoute KR, Schindler C;
PI Koong AC;
XX
XX WPI; 1999-580418/49.
DR P-PSDB; AAY42135.
XX
XX New isolated hypoxia-inducible genes, used to develop products for
PT diagnosis and treatment of hypoxia-related conditions, e.g. cancer,
PT ischaemia, reperfusion, retinopathy, neonatal distress, pre-eclampsia,
PT cardiac arrest or stroke -
XX
XX Claim 1; Fig 2; 109pp; English.
XX
CC The present sequence represents the human hypoxia-inducible gene HIG2.
CC Methods from the present invention can be used for identifying genes
CC inducible or repressible by stress, e.g. hypoxia, ionizing radiation,
CC hypothermia or heat shock. They can also be used for the diagnosis and
CC treatment of hypoxia related conditions e.g. cancer, ischaemia,
CC reperfusion, retinopathy, neonatal distress, pre-eclampsia, cardiac
CC arrest, or stroke,
XX
XX Sequence 1466 BP; 345 A; 357 C; 392 G; 372 T; 0 other;
SQ

Query Match 2.0%; Score 24; DB 20; Length 1466;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1150 tatttcaaaaaaaaaaaaaaaa 1173
|||||
DB 1417 tatttcaaaaaaaaaaaaaaaa 1440
|||||

RESULT 25
AAD03429
ID AAD03429 standard; cDNA; 1466 BP.
XX
AC AAD03429;
XX
DT 13-JUN-2001 (first entry)
XX
DE Human hypoxia-inducible gene, HIG2 cDNA.
XX
KW Human; hypoxia-inducible gene; HIG1; HIG2; antiischaemic; preeclampsia;
KW cytosolic; cerebroprotective; cardiac; ophthalmological; retinopathy;
KW reperfusion; neonatal distress; cardiac arrest; stroke; wound healing;
KW cancer; ischaemia; drug screening; ss.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 274..465
FT /*tag= a
FT /product= "Human HIG2 protein"
FT
PN WO200123426-A2.
XX
XX 05-APR-2001.
XX
XX 02-OCT-2000; 2000WO-US27189.
PF
XX
XX 30-SEP-1999; 98US-0410375.
XX
XX (VARI) VARIAN ASSOC INC.
PA
XX Denko NC, Giaccia AJ, Green CJ, Laderoute KR, Schindler C;
PI

PI Koong AC;
XX
DR WPI; 2001-226926/23.
DR P-PSDB; AAE00286.
XX
XX New assays, useful for determining the presence of hypoxia and for
PT evaluating a hypoxia-related condition in an animal, comprises
PT hypoxia-inducible genes, hypoxia-inducible polypeptides (HIP) or
PT antibodies immunoreactive with HIP -
XX
XX Example 3; Fig 2A; 110pp; English.
XX
CC The present cDNA sequence encodes human hypoxia-inducible protein, HIG2.
CC The invention relates to human hypoxia-inducible genes (HIG) such as
CC HIG1, HIG2, and their corresponding protein molecules. HIG proteins are
CC useful for treating hypoxia-related conditions such as ischaemia,
CC reperfusion, retinopathy, neonatal distress, preeclampsia, cardiac
CC arrest, cardiac stroke, wound healing and cancer, by attenuating the
CC hypoxic response of a tissue in an animal such as human. Protein
CC expression products of HIG are useful for diagnosing and screening drugs
CC for the treatment of hypoxia-related conditions. Immunoreactive HIG
CC antibodies are useful for isolating HIG1 and HIG2 from cells or
CC biological fluids. The invention also relates to methods for assaying the
CC expression of HIG, for determining the presence of hypoxia and for
CC evaluating the hypoxia-related condition. Methods are also provided for
CC identifying the stress-inducible and stress-repressible genes.
XX
XX Sequence 1466 BP; 345 A; 357 C; 392 G; 372 T; 0 other;
SQ

Query Match 2.0%; Score 24; DB 22; Length 1466;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1150 tatttcaaaaaaaaaaaaaaaa 1173
|||||
DB 1417 tatttcaaaaaaaaaaaaaaaa 1440
|||||

RESULT 26
AAD09829
ID AAD09829 standard; cDNA; 1928 BP.
XX
AC AAD09829;
XX
DT 12-SEP-2001 (first entry)
XX
DE Soybean SPFI-related transcription factor #5 cDNA.
XX
KW Soybean; SPFI-related transcription factor; transgenic plant;
KW genetical mapping; physical mapping; plant breeding; ss.
XX
OS Glycine max.
FH Key Location/Qualifiers
FT CDS 12..1739
FT /*tag= a
FT /product= "SPFI-related transcription factor #5"
FT
PN WO200149840-A2.
XX
XX 12-JUL-2001.
XX
XX 22-DEC-2000; 2000WO-US35310.
PF
XX
XX 04-JAN-2000; 2000US-0174325.
PR
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX
XX Zhu Q, Famodu OO, Rafalski JA;
PI
XX WPI; 2001-441876/47.
DR
DR P-PSDB; AAE05092.

XX Novel isolated SPF-1 related transcription factor polypeptides and
PT polynucleotides useful for producing transgenic plants -
XX
XX Claim 7: Page 52-53; 60pp; English.
XX
XX The present sequence is soybean SPFI-related transcription factor #5
CC cDNA. The SPFI-related transcription factor is useful for transforming a
CC cell by introducing SPFI-related transcription factor into a cell. It is
CC also useful for producing a transgenic plant by transforming a plant cell
CC with SPFI-related transcription factor and regenerating a plant from the
CC transformed plant cell. It is also useful to create transgenic plants in
CC which SPFI-related transcription factor DNA is present at higher or lower
CC levels than normal or in cell types or developmental stages in which they
CC are not normally found. The SPFI-related transcription factor DNA is
CC useful to prepare antibodies. It is also used as probes for genetically
CC and physically mapping the genes that they are a part of, and used as
CC markers for traits linked to these genes. Such information is useful in
CC plant breeding in order to develop lines with desired phenotype.
XX
XX Sequence 1928 BP; 591 A; 454 C; 387 G; 496 T; 0 other;
XX
XX
XX Query Match 2.0%; Score 24; DB 22; Length 1928;
XX Best Local Similarity 100.0%; Pred. No. 4.4;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1150 tatttcaaaaaaaaaaaaaaaaaa 1173
XX |
XX Db 1905 tatttcaaaaaaaaaaaaaaaaaa 1928
XX
XX
XX RESULT 27
XX AAC59457
XX ID AAC59457 standard; cDNA; 2254 BP.
XX
XX AC AAC59457;
XX
XX DT 26-JAN-2001 (first entry)
XX
XX DE Human secreted protein gene 9 SEQ ID NO:19.
XX
XX Human; secreted protein; diagnosis; antiarthritic; immunosuppressive;
XX antiarthritis; antiproliferative; cytostatic; cardiant; vasotrophic;
XX cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;
XX fungicide; ophthalmological; vulnary; gene therapy; autoimmune disease;
XX hyperproliferative disorder; neoplasia; cancer; cardiovascular disorder;
XX cerebrovascular disorder; angiogenesis; nervous system disorder;
XX infection; ocular disorder; wound healing; skin aging; food additive;
XX preservative; ss.
XX
XX Homo sapiens.
XX
XX OS WO200056755-A1.
XX
XX PD 28-SEP-2000.
XX
XX PF 16-MAR-2000; 2000WO-US06830.
XX
XX PR 19-MAR-1999; 99US-0125361.
XX
XX PR 10-DEC-1999; 99US-0169910.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM, Komatsoulis G;
XX
XX WPI: 2000-587661/35.
XX
XX P-PSDB; AAB34100.
XX
XX New isolated nucleic acid molecules encoding 49 human secreted proteins
XX used for preventing, treating or ameliorating medical conditions, for
XX diagnosing pathological conditions or as food additives or
XX preservatives -
XX

XX
PS Claim 1: Page 336-337; 419pp; English.
XX
XX The polynucleotide sequences given in AAC59449 to AAC59497 encode the
CC human secreted proteins given in AAB34092 to AAB34140. AAB34141 to
CC AAB34216 represent human secreted polypeptide sequences and proteins
CC homologous to them, which are given in the exemplification of the present
CC invention. Human secreted proteins have activities based on the tissue
CC and cells the genes are expressed in. Examples of activities include:
CC antiarthritic; immunosuppressive; antirheumatic; antiproliferative;
CC cytostatic; cardiant; vasotrophic; cerebroprotective; neurotropic;
CC neuroprotective; antibacterial; virucide; fungicide; ophthalmological;
CC and vulnary. The polynucleotides and polypeptides can be used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
CC in diagnosing a pathological condition or susceptibility to a
CC pathological condition. Disorders which are diagnosed or treated include
CC autoimmune diseases, hyperproliferative disorders e.g. neoplasms or
CC cancer of the breast or liver, cardiovascular disorders, cerebrovascular
CC disorders, angiogenesis, nervous system disorders, infections caused by
CC bacteria, viruses and fungi and ocular disorders. The polypeptides can
CC also be used to aid wound healing and epithelial cell proliferation, to
CC prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities. AAC59440 to AAC59448 and AAB34091 represent sequences used
CC in the exemplification of the present invention.
XX
XX Sequence 2254 BP; 721 A; 401 C; 410 G; 722 T; 0 other;
XX
XX
XX Query Match 2.0%; Score 24; DB 21; Length 2254;
XX Best Local Similarity 100.0%; Pred. No. 4.2;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1150 tatttcaaaaaaaaaaaaaaaaaa 1173
XX |
XX Db 1791 tatttcaaaaaaaaaaaaaaaaaa 1814
XX
XX
XX RESULT 28
XX AAQ12152
XX ID AAQ12152 standard; DNA; 2327 BP.
XX
XX AC AAQ12152;
XX
XX DT 24-SEP-1991 (first entry)
XX
XX DE Human transferrin gene.
XX
XX KW iron-binding protein; clone Tf; liver cDNA library; ss.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT sig_peptide 31..87
XX FT mat_peptide 88..2124
XX FT /tag= a
XX FT /tag= b
XX FT /product= transferrin
XX
XX PN US5026651-A.
XX
XX PD 25-JUN-1991.
XX
XX PF 25-APR-1985; 85US-0727335.
XX
XX PR 25-APR-1985; 85US-0727335.
XX
XX PA (TEXA) UNIV OF TEXAS SVST.
XX
XX X Bowman BH, Yang F;
XX

This invention describes novel recombinant human serum transferrin mutants with altered metal binding properties. The products of the invention act as iron chelators. The recombinant transferrins can be used in metal chelation therapy to bind and clear excess toxic metals in patients suffering from metal overloads. In particular transferrin mutants which bind iron with higher avidity than natural transferrin can be administered to individuals suffering from thalassemia to remove excess toxic iron from the body. Half-molecules or transferrin mutants with altered metal ion selectivities could be used to clear other toxic metals e.g. lead, mercury, cadmium copper or zinc from the body. Recombinant full length transferrin can also be used in non serum supplements or in tissue culture media. A transferrin half-molecule is advantageous as it is able to pass through the glomeruli of the kidney and can be excreted in the urine, unlike the holo-proteins, so that the metal is not only chelated but also cleared from the body. The single half-molecules do not bind to transferrin receptors on the membrane of tissue cells and therefore do not deliver the iron to these tissues. A further advantage is that the human body probably recognizes the half-molecules as 'self' and would not elicit an immunological response. Using recombinant transferrin avoids the risk of contamination with HIV or hepatitis virus associated with transferrin purified from human serum. This sequence encodes the human serum transferrin described in the invention.

Sequence 2327 BP; 623 A; 538 C; 627 G; 539 T; 0 other;

Query Match 2.0%; Score 24; DB 21; Length 2327;
Best Local Similarity 100.0%; Pred. No. 4.2; Mismatches 0; Indels 0; Gaps
Matches 24; Conservative 0;

QY 1150 tatttcacaaaaaaaaaaaaaa 1173
|||||
DB 2293 tatttcacaaaaaaaaaaaaaa 2316

RESULT 30
AAx76374
ID AAX76374 standard; cDNA; 2993 BP.
AC AC
XX AAX76374;
DT 05-AUG-1999 (first entry)
DE XX
DE XX
DE XX
KW Pneumocystis carinii isoleucyl-tRNA synthetase encoding cDNA.
KW pneumocystis carinii; lysyl-tRNA synthetase; tyrosyl-tRNA synthetase;
KW aminoacyl-tRNA synthetase; pneumonia; AIDS; immuno-compromised;
KW Acquired Immune Deficiency Syndrome; detection; ds.
XX XX
XX Pneumocystis carinii.
OS XX
XX Key Location/Qualifiers
CDS 1..2937
FT /*tag= a
ET
XX US5912140-A.
PN XX
PD XX
PD 15-JUN-1999.
PF 03-APR-1995; 95US-0415593.
PF XX
PF 03-APR-1995; 95US-0415593.
PR XX
PA (CUBI-) CUBIST PHARM INC.
PI Politis-Virk KI, Quinn CL, Schimmel PR, Tao N, Whoriskey SK;
PI WPI: 1999-357196/30.
DR P-PSDB; AAY17509.
DR XX
PT Nucleic acids encoding Pneumocystis carinii aminoacyl-tRNA

synthetase enzymes useful for detecting similar sequences in samples
 and in the study and treatment of pneumonia in Acquired Immune
 Deficiency Syndrome patients

Disclosure; Column 79-86; 66pp; English.

The present sequence encodes Pneumocystis carinii (P. carinii)
 isoleucyl-tRNA synthetase, which is an aminoacyl-tRNA synthetase enzyme.
 The nucleic acids encoding aminoacyl-tRNA synthetase enzymes may be used
 to produce expression vectors and host cells for the recombinant
 production of Pneumocystis aminoacyl-tRNA synthetases. The proteins may
 then be used in other procedures such as separating amino acids from
 samples or as antigens in the production of antibodies. The nucleic
 acids may also be used to produce tester cell strains (which contain the
 nucleic acids) which may be used to test candidate drugs (e.g. tRNA
 synthetase inhibitors) for the treatment of disorder associated with
 P. carinii such as pneumonia which is a common complication for Acquired
 Immune Deficiency Syndrome (AIDS) patients and other immuno-compromised
 individuals. Additionally, they may also be used to detect and isolate
 related DNAs in sample (i.e. they can be used as probes).

Sequence 2993 BP; 1042 A; 354 C; 561 G; 1036 T; 0 other;

Query Match 2.0%; Score 24; DB 20; Length 2993;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1150 tatttcaaaaaaaaaaaaaaaaaa 1173
 |||||
 Db 2963 tatttcaaaaaaaaaaaaaaaaaa 2986

RESULT 31

AAZ00877/c
 ID AAZ00877 standard; DNA; 24 BP.

AC AAZ00877;

XX 27-SEP-1999 (first entry)

DE PCR primer PGRT32 for PGI coding sequence.

XX PGI gene; biallelic marker; PCR primer; PGI-related biallelic marker;
 KW cancer; prostate cancer; diagnosis; therapy; prostate specific antigen;
 KW PSA; human; ss.

OS Synthetic.

OS Homo sapiens.

XX WO9932644-A2.

XX 01-JUL-1999.

XX 22-DEC-1998; 98WO-IB02133.

XX 09-SEP-1998; 98US-0099658.

XX 22-DEC-1997; 97US-0996306.

FA (GEST) GENSET.

XX Blumenfeld M, Bougueleret L, Chumakov I, Cohen D;

XX WPI; 1999-405178/34.

XX Use of a prostate cancer associated gene and biallelic markers
 derived from it

XX Example 6; Page 42; 385pp; English.

XX The invention relates to a mammalian PGI gene and protein, and a set of
 CC PGI biallelic markers. The PGI polynucleotide and biallelic markers are
 CC used in a hybridisation assay, a sequencing assay, or in an

CC allele-specific amplification assay for determining the identity of a
 CC nucleotide at a PGI-related biallelic marker. The methods can be used to
 CC detect and to assess the risk of developing cancer or prostate cancer.
 CC Early-stage diagnosis of prostate cancer relies on prostate specific
 CC antigen (PSA) dosage. However, the effectiveness of this is limited due
 CC to its inability to discriminate between malignant and non-malignant
 CC affections of the organ. A need exists for both a reliable diagnostic
 CC procedure which would enable early-stage diagnosis, and for preventative
 CC and curative treatments of the disease. The PGI gene can be used for
 CC detection of prostate cancer, and the risk of developing it in the
 CC future, and can also be used to determine therapies for the disease.

XX Sequence 24 BP; 3 A; 0 C; 1 G; 20 T; 0 other;

Query Match 2.0%; Score 23; DB 20; Length 24;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1151 atttcaaaaaaaaaaaaaaaaaa 1173

Db 24 ATTTCAAAAAAAAAAAAAAAAA 2

RESULT 32

AAQ86155/c

ID AAQ86155 standard; DNA; 42 BP.

XX AAQ86155;

XX AC

DT 21-NOV-1995 (first entry)

XX Sindbis polyA primer.

XX Eukaryotic layered vector initiation system; Sindbis; alphavirus; PCR;
 KW transcription initiation; non-structural protein; subgenomic fragment;
 KW RNA polymerase recognition sequence; ELVIS; gene therapy; amplify;
 KW primer; polymerase chain reaction; cystic fibrosis; ss.

OS Synthetic.

XX WO9507994-A.

XX 23-MAR-1995.

XX 15-SEP-1994; 94WO-US10469.

XX 15-SEP-1993; 93US-0122791.

XX 18-FEB-1994; 94US-0198450.

XX (VIAG-) VIAGENE INC.

XX Chang SMW, Driver DA, Dubensky TW, Ibanez CE, Jolly DJ;

XX Polo JM;

XX WPI; 1995-131362/17.

XX New alpha virus vectors for gene therapy - of viral infection,
 PT cancer, auto-immune disease, etc., and as vaccines.

XX Example 1; Page 58; 260pp; English.

XX The sequences given in AAQ86155-66 are primers which were used in the
 CC cloning of Sindbis genomic length cDNA for inclusion in a eukaryotic
 CC layered vector initiation system (ELVIS) derived from Sindbis. ELVIS's
 CC comprise a 5' sequence capable of initiating transcription of an
 CC alphavirus, a nucleotide sequence encoding alphavirus non-structural
 CC proteins, a viral junction region which has been inactivated such that
 CC viral transcription of the subgenomic fragment is prevented, and an
 CC alphavirus RNA polymerase recognition sequence. Inactivation of the
 CC viral junction region prevents transcription of the subgenomic
 CC fragment making vectors such as this suitable for a wide variety of
 CC applications, eg. gene therapy for the treatment of cystic fibrosis.

XX
SQ Sequence 42 BP; 7 A; 1 C; 3 G; 31 T; 0 other;

Query Match 2.0%; Score 23; DB 16; Length 42;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaa 1173
|||||

Db 41 ATTTCACAAAAA 19

RESULT 33
AAT35054/C
ID AAT35054 standard; cDNA; 42 BP.

XX AAT35054;
XX
XX 24-FEB-1997 (first entry)
XX
XX Sindbis virus strain AR-339 primer.

XX HSV; herpes simplex virus; solid tumour; killing; cancer; metastasis;
KW neovascularisation; angiogenesis; blood clot; neoplasia; viral vector;
KW gene therapy; ss.

XX Synthetic.
XX
XX WO9621416-A2.
XX
XX 18-JUL-1996.
XX
XX 22-DEC-1995; 95WO-US16855.
XX
XX 30-DEC-1994; 94US-0368574.
XX
XX (CHIR) CHIRON VIAGENE INC.

XX Burrows FJ, Dubensky TW, Fong TC, Jolly DJ, Polo JM;
XX WPI; 1996-342012/34.

XX Transducing cells in or adjacent to a tumour with a gene delivery
PT vehicle - useful to kill cells in vivo, inhibit tumour
PT angiogenesis, etc.

XX Example 1; Page 40; 159pp; English.

XX AAT35054 is a PCR primer used to amplify genomic length Sindbis cDNA
CC which is used in the construction of a Sindbis viral vector. The
CC vector may be used to transduce cells in or adjacent to a tumour
CC to inhibit tumour cell growth. The vector may express a protein
CC capable of killing tumour cells by activating a non-cytotoxic agent
CC into a cytotoxic one (e.g. herpes simplex virus (HSV)-1 thymidine
CC kinase). Such a vector can be used to transduce cells of a blood
CC vessel in or adjacent to an arterial side of a tumour. The invention
CC includes other viral vectors expressing other tumour-killing or
CC inhibiting agents, e.g. blood clotting factors (cut off the tumours
CC blood supply), angiogenesis inhibitors (inhibit vascularisation of
CC the tumour) and proteins that render nutrients in the perivascular
CC space of a tumour unusable (by binding to or metabolising the
CC nutrients).

XX Sequence 42 BP; 7 A; 1 C; 3 G; 31 T; 0 other;

Query Match 2.0%; Score 23; DB 17; Length 42;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaa 1173
|||||

Db 41 ATTTCACAAAAA 19

RESULT 34
AAT30789/C
ID AAT30789 standard; DNA; 42 BP.

XX AAT30789;
XX
XX 12-SEP-1996 (first entry)
XX
XX Sindbis genomic cDNA primer 4B.

XX Alphavirus; Sindbis virus; vector; gene therapy; vaccine;
KW primer; polymerase chain reaction; PCR; ss.
XX Synthetic.

XX WO9617072-A2.
XX
XX 06-JUN-1996.
XX
XX 30-NOV-1995; 95WO-US15490.

XX 15-MAR-1995; 95US-0405827.
XX 30-NOV-1994; 94US-0348472.
XX 18-JAN-1995; 95US-0376184.

XX (CHIR) CHIRON VIAGENE INC.

XX Belli BA, Chang SMW, Driver DA, Dubensky TW, Ibanez CE;
PI Jolly DJ, Polo JM;
XX WPI; 1996-277785/28.

XX New recombinant alpha-virus vectors - used to develop prods and
PT methods for use in gene therapy and in the prodn. of vaccines

XX Example 1; Page 59; 256pp; English.

XX An oligonucleotide primer (AAT30789) contains at its 5' end a
CC buffer sequence for efficient restriction endonuclease digestion,
CC a XhoI site, 25 nt nucleotides, and 6 nucleotides that are
CC precisely complementary to the extreme 3' end (nts 11698-11703)
CC of Sindbis virus. It was used for first strand cDNA synthesis from
CC polyA mRNA obtd. from virions of Sindbis virus strain Ar-338 (ATCC
CC VR 1248) propagated in BHK cells. It was also used for the PCR
CC amplification of Sindbis genomic cDNA (see also AAT30790-800) to
CC produce cDNA clone pVSP6GEN useful for vector construction (see
CC also AAT30787).

XX Sequence 42 BP; 7 A; 1 C; 3 G; 31 T; 0 other;

Query Match 2.0%; Score 23; DB 17; Length 42;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaa 1173
|||||

Db 41 ATTTCACAAAAA 19

RESULT 35
AAV60127/C
ID AAV60127 standard; DNA; 42 BP.

XX AAV60127;
XX
XX 04-DEC-1998 (first entry)

XX PCR primer 4B used to produce Sindbis virus cDNA.
XX

KW Eukaryotic layered vector initiation system; stimulate; immune response;
KW PCR primer; ss.

XX Synthetic.
OS Sindbis virus.

XX PN US5814482-A.
XX PD 29-SEP-1998.

XX PF 30-OCT-1996; 96US-0739158.
XX PR 15-SEP-1993; 93US-0122791.
XX PR 18-FEB-1994; 94US-0198450.
XX PR 14-SEP-1994; 94WO-US10469.
XX PR 30-NOV-1994; 94US-0348472.
XX PR 18-JAN-1995; 95US-0376184.
XX PR 30-OCT-1996; 96US-0739158.

XX PA (DRIV/) DRIVER D A.
XX PA (DUBE/) DUBENSKY T W.
XX PA (JOLLY/) JOLLY D J.
XX PA (POLO/) POLO J M.

XX PI Driver DA, Dubensky TW, Jolly DJ, Polo JM;
XX PD WPT; 1998-541753/46.

XX Eukaryotic layered vector initiation system - containing eukaryotic
PT promoter and heterologous antigen coding sequence, useful for
PT stimulating immune response
XX Example 1; Column 51; 144pp; English.
XX PCR primers AAV60127-38 were used to produce and amplify Sindbis
CC cDNA. This is then used to produce an eukaryotic layered vector
CC initiation system. The eukaryotic layered vector initiation
CC system comprises a eukaryotic promoter 5' of viral cDNA which
CC initiates, in a susceptible target cell, 5' to 3' synthesis of
CC RNA from the viral cDNA. The RNA comprises a vector construct which
CC autonomously amplifies in the cell and expresses a heterologous nucleic
CC acid sequence which encodes an antigen or modified form that stimulates
CC an immune response within an animal. The system is useful for
CC stimulating an immune response to an antigen by introducing the vector
CC into target cells, preferably by infection in vivo, especially where the
CC immune response is a cell mediated, HLA class I-restricted or an HLA
CC class II-restricted immune response.
XX Sequence 42 BP; 7 A; 1 C; 3 G; 31 T; 0 other;

XX Query Match 2.0%; Score 23; DB 19; Length 42;
XX Best Local Similarity 100.0%; Pred. No. 21;
XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1151 atttcaaaaaaaaaaaaaaaaa 1173
XX DB 41 ATTTCAAAAAAAAAAAAAAAAA 19

XX RESULT 36
XX AAV42366/c
XX ID AAV42366 standard; DNA; 42 BP.

XX AC AAV42366;
XX XX

XX DT 02-OCT-1998 (first entry)
XX DE PCR primer 4B used to amplify Sindbis cDNA.

XX KW DNA alphavirus; structural protein expression; inhibit; pathogen;
KW immune response; stimulate; PCR primer; ss.
XX

OS Synthetic.
OS Sindbis virus.

XX PN US5789245-A.
XX PD 04-AUG-1998.

XX PF 30-OCT-1996; 96US-0741881.
XX PR 15-MAR-1995; 95US-0404796.
XX PR 15-SEP-1993; 93US-0122791.
XX PR 18-FEB-1994; 94US-0198450.
XX PR 30-NOV-1994; 94US-0348472.
XX PR 20-JAN-1995; 95US-0376184.
XX PR 30-OCT-1996; 96US-0741881.

XX PA (CHIR) CHIRON CORP.
XX PI Chang SMW, Driver DA, Dubensky TW, Ibanez CE, Jolly DJ;
XX PI Polo JM;

XX DR WPI; 1998-446089/38.
XX PT DNA alpha:virus structural protein expression cassettes - for
XX PT producing recombinant alpha:virus particles
XX PS Example 1; Column 52; 140pp; English.

XX PCR primers AAV42367-420 and AAV42422-54 are used in the course of the
CC invention. The specification describes a DNA alphavirus structural
CC protein expression cassette which comprises an inducible promoter and
CC an alphavirus structural protein gene, where the promoter directs the
CC expression of the alphavirus structural protein gene upon induction of
CC the promoter within a cell, and where prior to induction within the
CC cell, the expression cassette does not express sufficient quantities of
CC structural proteins to be cytotoxic to a BHK cell containing the
CC expression cassette. The products may be used to inhibit pathogens and
CC stimulate an immune response.
XX Sequence 42 BP; 7 A; 1 C; 3 G; 31 T; 0 other;

XX Query Match 2.0%; Score 23; DB 19; Length 42;
XX Best Local Similarity 100.0%; Pred. No. 21;
XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1151 atttcaaaaaaaaaaaaaaaaa 1173
XX DB 41 ATTTCAAAAAAAAAAAAAAAAA 19

XX RESULT 37
XX AAV70686/c
XX ID AAV70686 standard; DNA; 42 BP.

XX AC AAV70686;
XX XX

XX DT 02-FEB-1999 (first entry)
XX DE Primer 4B used to produce Sindbis virus cDNA from mRNA.

XX KW Alphavirus vector construct; gene therapy; primer; ss.
XX OS Synthetic.
XX OS Sindbis virus.

XX PN US5843723-A.
XX PD 01-DEC-1998.

XX PF 30-OCT-1996; 96US-0739167.
XX PR 20-MAR-1995; 95US-0404796.

PR 15-SEP-1993; 93US-0122791.
 PR 18-FEB-1994; 94US-0198450.
 PR 30-NOV-1994; 94US-0348472.
 PR 20-JAN-1995; 95US-0376184.
 PR 30-OCT-1996; 96US-0739167.

XX (CHIR) CHIRON CORP.

XX Belli BA, Chang SMW, Driver DA, Dubensky TW, Ibanez CE;

PI Jolly DJ, Polo JM;

XX WPI; 1999-044581/04.

XX Alphavirus vectors constructs containing a 5' promoter of viral cDNA
 PT by in vitro transcription - used in gene therapy

XX Example 1; Column 52; 140pp; English.

XX The present primer was used to produce Sindbis virus cDNA from
 CC mRNA. The Sindbis cDNA was then amplified to produce a
 CC genomic length Sindbis cDNA sequence, which was then used to create
 CC the alphavirus vector constructs of the invention. These constructs
 CC comprise a promoter 5' of viral cDNA which initiates the synthesis
 CC of RNA from the viral cDNA by in vitro transcription, followed by
 CC a 5' sequence which initiates transcription of alphavirus RNA,
 CC followed by a nucleotide sequence encoding alphavirus nonstructural
 CC proteins, a viral junction region which has been inactivated such that
 CC viral transcription of a subgenomic fragment is prevented, an internal
 CC ribosome entry site or a sequence which promotes ribosome read through
 CC between adjacent reading frames, and an alphavirus RNA polymerase
 CC recognition sequence. The recombinant alphavirus vectors can be used
 CC for gene therapy.

XX Sequence 42 BP; 7 A; 1 C; 3 G; 31 T; 0 other;

Query Match 2.0%; Score 23; DB 20; Length 42;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaaa 1173
 |||||
 Db 41 ATTTCAAAAAAAAAAAAAAAAAA 19

RESULT 38
 AAZ92767/c
 ID AAZ92767 standard; DNA; 42 BP.

XX AC AAZ92767;

XX DT 22-MAY-2000 (first entry)

XX Sindbis virus genomic cDNA PCR primer SEQ ID NO:3.

XX Recombinant alphavirus vector; gene therapy; anticancer; antiviral;
 KW eukaryotic layered vector initiation system; antimicrobial; cardiant;
 KW antidiabetic; antineurodegeneration; immunomodulatory; immune response;
 KW infection; melanoma; cancer; diabetes; autoimmune disorder;
 KW graft versus host disease; Alzheimer's disease; heart disease;
 KW haemophilia; cystic fibrosis; PCR primer; ss.

XX Sindbis virus.

XX US6015686-A.

XX PD 18-JAN-2000.

XX PF 15-MAR-1995; 95US-0404796.

XX PR 15-SEP-1993; 93US-0122791.

PR 18-FEB-1994; 94US-0198450.

PR 30-NOV-1994; 94US-0348472.

PR 20-JAN-1995; 95US-0376184.

XX (CHIR) CHIRON VIAGENE INC.

XX Polo JM, Jolly DJ, Driver DA, Dubensky TW;

XX WPI; 2000-181143/16.

XX Eukaryotic layered vector initiation system useful for gene therapy and
 PT production of recombinant protein, comprises promoter that directs
 PT synthesis of RNA containing a vector construct -

XX Example 1; Column 51; 141pp; English.

XX The present invention describes a eukaryotic layered vector initiation
 CC system (A) comprising a eukaryotic promoter (EP), 5' of viral cDNA (I)
 CC which initiates the 5' to 3' synthesis of RNA (II) from (I). (II)
 CC comprises a vector construct (VC), expressing a heterologous nucleic
 CC acid (III), which amplifies autonomously in a cell. (A) can have
 CC anticancer, antiviral, antimicrobial, antidiabetic, immunomodulatory,
 CC antineurodegeneration and cardiant activities. (A) are used to express
 CC therapeutic proteins in cell cultures; in gene therapy (for humans or
 CC animals), e.g. to induce a specific immune response; to inhibit
 CC interaction of an agent with cellular receptors; to express a toxin;
 CC to regulate the immune system or to express a replacement gene, e.g.
 CC for treatment or prevention of infections (by viruses or other
 CC pathogens), melanoma (or other cancers), diabetes (or other autoimmune
 CC disorders), graft versus host disease, Alzheimer's disease, heart
 CC disease, haemophilia, cystic fibrosis and many others; or for production
 CC of packaged vector particles (also useful for gene therapy). (A) can
 CC also be used to produce transgenic plants that express resistance or
 CC growth promoting sequences. AAZ92765 to AAZ92891 and AAZ92891 to AAZ92891 represent
 CC sequences used in the exemplification of the present invention.

XX Sequence 42 BP; 7 A; 1 C; 3 G; 31 T; 0 other;

Query Match 2.0%; Score 23; DB 21; Length 42;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaaa 1173
 |||||
 Db 41 ATTTCAAAAAAAAAAAAAAAAAA 19

RESULT 39
 AAZ92894/c
 ID AAZ92894 standard; DNA; 42 BP.

XX AC AAZ92894;

XX DT 22-MAY-2000 (first entry)

XX Sindbis virus genomic cDNA PCR primer SEQ ID NO:3.

XX Recombinant alphavirus vector; gene therapy; anticancer; antiviral;
 KW eukaryotic layered vector initiation system; antimicrobial; cardiant;
 KW antidiabetic; antineurodegeneration; immunomodulatory; immune response;
 KW infection; melanoma; cancer; diabetes; autoimmune disorder;
 KW graft versus host disease; Alzheimer's disease; heart disease;
 KW haemophilia; cystic fibrosis; PCR primer; ss.

XX Sindbis virus.

XX US6015694-A.

XX PD 18-JAN-2000.

XX PF 16-SEP-1997; 97US-0931869.

XX PR 15-MAR-1995; 95US-0404796.

PR 15-SEP-1993; 93US-0122791.

PR 18-FEB-1994; 94US-0198450.

PR 30-NOV-1994; 94US-0348472.
 PR 18-JAN-1995; 95US-0376184.
 PA (CHIR) CHIRON CORP.
 XX Jolly DJ, Chang SM, Polo JM, Dubensky TW;
 XX WPI; 2000-181146/16.
 DR
 XX Stimulating an immune response in an animal, useful e.g. for protecting
 PT against viruses or tumors, by infecting target cells with recombinant
 PT alphavirus particles that express an antigen -
 XX
 XX Example 1; Column 52; 140pp; English.
 XX
 CC The present invention describes a method for stimulating, in an animal,
 CC an immune response to an antigen (Ag). The method comprises infecting
 CC target cells in the animal with recombinant alphavirus particles (AVP)
 CC that direct expression of at least one Ag, optionally modified, in the
 CC infected cells. AVP are derived from an alphavirus packaging cell line
 CC comprising a stably transformed expression cassette (EC) which expresses
 CC an alphavirus structural protein that is able, after introduction of an
 CC alphavirus vector construct (AVC), to produce recombinant AVP or the
 CC AVPs are free from recombinant AVPs that can initiate productive
 CC infection to produce infectious AVPs. The method is used, in human or
 CC veterinary medicine, to induce an immune response, particularly
 CC cell-mediated or HLA (human leucocyte antigen) Class I or II restricted,
 CC e.g. against viruses (especially hepatitis C), tumours, bacteria,
 CC parasites or fungi. Cells infected with alphavirus particles are fully
 CC viable and present antigens efficiently; the antigenic epitopes exposed
 CC can be altered by selective cloning of gene subfragments (including
 CC expression of multiple epitopes), and they effectively stimulate
 CC cytotoxic T cells. AA292892 to AA293018 and AA293017 represent sequences
 CC used in the exemplification of the present invention.
 XX
 XX Sequence 42 BP; 7 A; 1 C; 3 G; 31 T; 0 other;
 SQ

Query Match 2.0%; Score 23; DB 21; Length 42;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1151 attcaaaaaaiaaaaaaaaaa 1173
 Db 41 ATTTCAAAAAAAAAAAAAAAAAA 19

RESULT 40
 AAQ86183/c
 ID AAQ86183 standard; DNA; 48 BP.
 XX
 XX AAQ86183;
 AC
 XX 23-NOV-1995 (first entry)
 DT
 XX Primer S1NXball700R amplifies plasmid DNA sindbis basic vector.
 DE
 XX Eukaryotic layered vector initiation system: Sindbis; alphavirus; PCR;
 XX transcription initiation; non-structural protein; subgenomic fragment;
 KW RNA polymerase recognition sequence; ELVIS; gene therapy; amplify;
 KW primer; polymerase chain reaction; cystic fibrosis; ss.
 XX
 XX Synthetic.
 OS
 XX WO9507994-A.
 PN
 XX 23-MAR-1995.
 PD
 XX 15-SEP-1994; 94WO-US10469.
 XX
 XX 15-SEP-1993; 93US-0122791.
 PR
 PR 18-FEB-1994; 94US-0198450.
 XX

PA (VIAG-) VIAGENE INC.
 XX Chang SMW, Driver DA, Dubensky TW, Ibanez CE, Jolly DJ;
 PI Polo JM;
 XX WPI; 1995-131362/17.
 DR
 XX New alpha virus vectors for gene therapy - of viral infection,
 PT cancer, auto-immune disease, etc., and as vaccines.
 PT
 PS Example 3; Page 74; 260pp; English.
 XX
 CC The sequences given in AAQ86182-85 are primers which were used in the
 CC generation of plasmid DNA sindbis basic vectors. The amplified DNA
 CC sequences were used in the construction of a eukaryotic layered vector
 CC initiation system (ELVIS) derived from Sindbis. ELVIS's comprise a 5'
 CC sequence capable of initiating transcription of an alphavirus, a
 CC nucleotide sequence encoding alphavirus non-structural proteins, a
 CC viral junction region which has been inactivated such that viral
 CC transcription of the subgenomic fragment is prevented, and an
 CC alphavirus RNA polymerase recognition sequence. Inactivation of the
 CC viral junction region prevents transcription of the subgenomic
 CC fragment making vectors such as this suitable for a wide variety of
 CC applications, eg. gene therapy for the treatment of cystic fibrosis.
 XX
 XX Sequence 48 BP; 10 A; 2 C; 4 G; 32 T; 0 other;
 SQ

Query Match 2.0%; Score 23; DB 16; Length 48;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1151 attcaaaaaaiaaaaaaaaaa 1173
 Db 41 ATTTCAAAAAAAAAAAAAAAAAA 19

RESULT 41
 AAT35073/c
 ID AAT35073 standard; cDNA; 48 BP.
 XX
 XX AAT35073;
 AC
 XX 24-FEB-1997 (first entry)
 DT
 XX Sindbis-based, tumour inhibiting, viral vector construction primer.
 DE
 XX HSV; herpes simplex virus; solid tumour; killing; cancer; metastasis;
 KW neovascularisation; angiogenesis; blood clot; neoplasia; viral vector;
 KW gene therapy; ss.
 KW
 XX Synthetic.
 OS
 XX WO9621416-A2.
 PN
 XX 18-JUL-1996.
 PD
 XX 22-DEC-1995; 95WO-US16855.
 XX
 XX 30-DEC-1994; 94US-0368574.
 PR
 XX (CHIR) CHIRON VIAGENE INC.
 PA
 XX Burrows FJ, Dubensky TW, Fong TC, Jolly DJ, Polo JM;
 PI WPI; 1996-342012/34.
 XX
 XX Transducing cells in or adjacent to a tumour with a gene delivery
 PT vehicle - useful to kill cells in vivo, inhibit tumour
 PT angiogenesis, etc.
 XX
 XX Example 1; Page 50; 159pp; English.
 PS
 XX

CC AAT35072-T35075 are PCR primers used in the construction of Sindbis-
 CC based viral vectors which can be used to transduce cells in or adjacent
 CC to a tumour to inhibit tumour cell growth. The vectors express a
 CC protein capable of killing tumour cells by activating a non-cytotoxic
 CC agent into a cytotoxic one (e.g. herpes simplex virus (HSV)-1 thymidine
 CC kinase). Such a vector can be used to transduce cells of a blood vessel
 CC in or adjacent to an arterial side of a tumour. The invention includes
 CC other viral vectors expressing other tumour-killing or inhibiting
 CC agents, e.g. blood clotting factors (cut off the tumours blood supply),
 CC angiogenesis inhibitors (inhibit vascularisation of the tumour) and
 CC proteins that render nutrients in the perivascular space of a tumour
 CC unusable (by binding to or metabolising the nutrients).
 XX
 SQ Sequence 48 BP; 10 A; 2 C; 4 G; 32 T; 0 other;

Query Match 2.0%; Score 23; DB 17; Length 48;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaaa 1173
 |||||
 Db 41 ATTTCAAAAAAAAAAAAAAAAAA 19

RESULT 42

AAT30807/C
 ID AAT30807 standard; DNA; 48 BP.

XX
 AC AAT30807;

XX
 DT 12-SEP-1996 (first entry)

XX
 DE Sindbis PCR primer SINSac11700R.

XX
 KW Alphavirus; Sindbis virus; vector; gene therapy; vaccine;
 KW primer; polymerase chain reaction; PCR; pKSSINBV; ss.

XX
 OS Synthetic.

XX
 PN WO9617072-A2.

XX
 PD 06-JUN-1996.

XX
 PF 30-NOV-1995; 95WO-0515490.

XX
 PR 15-MAR-1995; 95US-0405827.

XX
 PR 30-NOV-1994; 94US-0348472.

XX
 PR 18-JAN-1995; 95US-0376184.

XX
 PA (CHIR) CHIRON VIAGENE INC.

XX
 PI Belli BA, Chang SMW, Driver DA, Dubensky TW, Ibanez CE;

XX
 PI Jolly DJ, Polo JM;

XX
 DR WPI; 1996-277785/28.

XX
 PT New recombinant alpha-virus vectors - used to develop prods and
 PT methods for use in gene therapy and in the prodn. of vaccines

XX
 PS Example 3; Page 68; 256pp; English.

XX
 CC Reverse primer SINSac11700R (AAT30807) has a buffer sequence for
 CC efficient restriction endonuclease digestion, a SacI site, and
 CC a sequence complementary to nucleotides 11700-11692 of Sindbis
 CC genomic DNA. It was mixed with forward primer SIN11664F (AAT30806)
 CC and the product was ligated into pKS II+. A plasmid subclone,
 CC pKSI13/SIN, was obtd. that contained the 40 terminal nucleotides of
 CC the viral 3' end and a 25 bp stretch of dA:dt nucleotides. This
 CC was ligated with a subclone contg. Sindbis nucleotides 1-7643 (see
 CC also AAT30808) to create Sindbis basic vector pKSSINBV, useful in the
 CC construction of recombinant vectors useful for gene therapy and
 CC vaccine prodn.

XX
 SQ Sequence 48 BP; 10 A; 2 C; 4 G; 32 T; 0 other;

Query Match 2.0%; Score 23; DB 17; Length 48;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaaa 1173
 |||||
 Db 41 ATTTCAAAAAAAAAAAAAAAAAA 19

RESULT 43

AAV42384/C
 ID AAV42384 standard; DNA; 48 BP.

XX
 AC AAV42384;

XX
 DT 02-OCT-1998 (first entry)

XX
 DE Reverse PCR primer SINSac1700R.

XX
 KW DNA alphavirus; structural protein expression; inhibit; pathogen;
 KW immune response; stimulate; PCR primer; ss.

XX
 OS Synthetic.

XX
 PN US5789245-A.

XX
 PD 04-AUG-1998.

XX
 PF 30-OCT-1996; 96US-0741881.

XX
 PR 15-MAR-1995; 95US-0404796.

XX
 PR 18-FEB-1994; 94US-0122791.

XX
 PR 30-NOV-1994; 94US-0348472.

XX
 PR 20-JAN-1995; 95US-0376184.

XX
 PR 30-OCT-1996; 96US-0741881.

XX
 PA (CHIR) CHIRON CORP.

XX
 PI Chang SMW, Driver DA, Dubensky TW, Ibanez CE, Jolly DJ;

XX
 PI Polo JM;

XX
 DR WPI; 1998-446089/38.

XX
 PT DNA alpha:virus structural protein expression cassettes - for
 PT producing recombinant alpha:virus particles

XX
 PS Example 3; Column 57; 140pp; English.

XX
 CC PCR primers AAV42367-420 and AAV42422-54 are used in the course of the
 CC invention. The specification describes a DNA alphavirus structural
 CC protein expression cassette which comprises an inducible promoter and
 CC an alphavirus structural protein gene, where the promoter directs the
 CC expression of the alphavirus structural protein gene upon induction of
 CC the promoter within a cell, and where prior to induction within the
 CC cell, the expression cassette does not express sufficient quantities of
 CC structural proteins to be cytotoxic to a BHK cell containing the
 CC expression cassette. The products may be used to inhibit pathogens and
 CC stimulate an immune response.

XX
 SQ Sequence 48 BP; 10 A; 2 C; 4 G; 32 T; 0 other;

Query Match 2.0%; Score 23; DB 19; Length 48;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaaa 1173
 |||||

Db 41 ATTTCAAAAAAAAAAAAAAAAAAAAA 19

RESULT 44

AAV70704/c

ID AAV70704 standard; DNA; 48 BP.

XX AC AAV70704;

XX 02-FEB-1999 (first entry)

XX DE Reverse PCR primer SINSac 11700R for Sindbis virus 3' end.

XX KW Alphavirus vector construct; gene therapy; PCR primer; ss.

XX OS Synthetic.

XX OS Sindbis virus.

XX PN US5843723-A.

XX PD 01-DEC-1998.

XX PF 30-OCT-1996; 96US-0739167.

XX PR 20-MAR-1995; 95US-0404796.

XX PR 15-SEP-1993; 93US-0122791.

XX PR 18-FEB-1994; 94US-0198450.

XX PR 30-NOV-1994; 94US-0348472.

XX PR 20-JAN-1995; 95US-0376184.

XX PR 30-OCT-1996; 96US-0739167.

XX PA (CHIR) CHIRON CORP.

XX PI Belli BA, Chang SMW, Driver DA, Dubensky TW, Ibanez CE;

XX PI Jolly DJ, Polo JM;

XX WPI; 1999-044581/04.

XX Alphavirus vectors containing a 5' promoter of viral cDNA

XX by in vitro transcription - used in gene therapy

XX Example 3; Column 57; 140pp; English.

XX PCR primers AAV70703-05 are used to amplify the 3' end of Sindbis virus.

XX The amplified product is used in the production of the alphavirus vector

XX constructs of the invention. These constructs comprise a promoter 5' of

XX viral cDNA which initiates the synthesis of RNA from the viral cDNA by

XX in vitro transcription, followed by a 5' sequence which initiates

XX encoding alphavirus nonstructural proteins, a viral junction region

XX which has been inactivated such that viral transcription of a subgenomic

XX fragment is prevented, an internal ribosome entry site or a sequence

XX which promotes ribosome read through between adjacent reading frames,

XX and an alphavirus RNA polymerase recognition sequence. The recombinant

XX alphavirus vectors can be used for gene therapy.

XX Sequence 48 BP; 10 A; 2 C; 4 G; 32 T; 0 other;

XX Query Match 2.0%; Score 23; DB 20; Length 48;

XX Best Local Similarity 100.0%; Pred. No. 21;

XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaaaaaa 1173

Db 41 ATTTCAAAAAAAAAAAAAAAAAAAAA 19

RESULT 45

AAZ92785/c

ID AAZ92785 standard; DNA; 48 BP.

XX AC AAZ92785;

XX

DT 22-MAY-2000 (first entry)

DE Sindbis basic vector construction primer SEQ ID NO:21.

XX

KW Recombinant alphavirus vector; gene therapy; anticancer; antiviral;

KW eukaryotic layered vector initiation system; antimicrobial; cardiant;

KW antidiabetic; antineurodegeneration; immunomodulatory; immune response;

KW infection; melanoma; cancer; diabetes; autoimmune disorder;

KW graft versus host disease; Alzheimer's disease; heart disease;

KW haemophilia; cystic fibrosis; PCR primer; ss.

XX

OS Sindbis virus.

OS Synthetic.

XX

PN US6015686-A.

XX

PD 18-JAN-2000.

XX

PF 15-MAR-1995; 95US-0404796.

XX

PR 15-SEP-1993; 93US-0122791.

PR

PR 18-FEB-1994; 94US-0198450.

PR

PR 30-NOV-1994; 94US-0348472.

PR

PR 20-JAN-1995; 95US-0376184.

XX

PA (CHIR) CHIRON VIAGENE INC.

XX

PI Polo JM, Jolly DJ, Driver DA, Dubensky TW;

XX

WPI; 2000-181143/16.

XX

DR Eukaryotic layered vector initiation system useful for gene therapy and

XX

PT production of recombinant protein, comprises promoter that directs

PT synthesis of RNA containing a vector construct -

XX

PS Example 3; Column 57; 141pp; English.

XX

CC The present invention describes a eukaryotic layered vector initiation

CC system (A) comprising a eukaryotic promoter (EP), 5' of viral cDNA (I)

CC which initiates the 5' to 3' synthesis of RNA (II) from (I). (II)

CC comprises a vector construct (VC), expressing a heterologous nucleic

CC acid (III), which amplifies autonomously in a cell. (A) can have

CC anticancer, antiviral, antimicrobial, antidiabetic, immunomodulatory,

CC antineurodegeneration and cardiant activities. (A) are used to express

CC therapeutic proteins in cell cultures; in gene therapy (for humans or

CC animals), e.g. to induce a specific immune response; to inhibit

CC interaction of an agent with cellular receptors; to express a toxin;

CC to regulate the immune system or to express a replacement gene, e.g.

CC for treatment or prevention of infections (by viruses or other

CC pathogens), melanoma (or other cancers), diabetes (or other autoimmune

CC disorders), graft versus host disease, Alzheimer's disease, heart

CC disease, haemophilia, cystic fibrosis and many others; or for production

CC of packaged vector particles (also useful for gene therapy). (A) can

CC also be used to produce transgenic plants that express resistance or

CC growth promoting sequences. AAZ92765 to AAZ92891 and AAZ90146 represent

CC sequences used in the exemplification of the present invention.

XX

SQ Sequence 48 BP; 10 A; 2 C; 4 G; 32 T; 0 other;

Query Match 2.0%; Score 23; DB 21; Length 48;

Best Local Similarity 100.0%; Pred. No. 21;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaaaaaa 1173

Db 41 ATTTCAAAAAAAAAAAAAAAAAAAAA 19

RESULT 46

AAZ92912/c

ID AAZ92912 standard; DNA; 48 BP.

XX AAZ92912;
 XX 22-MAY-2000 (first entry)
 XX Sindsbis basic vector construction primer SEQ ID NO:21.
 XX Recombinant alphavirus vector; gene therapy; anticancer; antiviral;
 KW eukaryotic layered vector initiation system; antibacterial; HLA;
 KW antiparasitic; vaccine; immune response; cell-mediated; hepatitis C;
 KW human leucocyte antigen; tumour; bacteria; virus; parasite; fungal;
 KW infection; PCR primer; ss.
 XX Sindsbis virus.
 OS Synthetic.
 OS US6015694-A.
 XX 18-JAN-2000.
 XX 16-SEP-1997; 97US-0931869.
 XX 15-MAR-1995; 95US-0404796.
 PR 15-SEP-1993; 93US-0122791.
 PR 18-FEB-1994; 94US-0198450.
 PR 30-NOV-1994; 94US-0348472.
 PR 18-JAN-1995; 95US-0376184.
 XX (CHIR) CHIRON CORP.
 PA Jolly DJ, Chang SM, Polo JM, Dubensky TW;
 PI WPI; 2000-181146/16.
 DR Stimulating an immune response in an animal, useful e.g. for protecting
 PT against viruses or tumors, by infecting target cells with recombinant
 PT alphavirus particles that express an antigen -
 XX Example 3; Column 58; 140pp; English.
 XX The present invention describes a method for stimulating, in an animal,
 CC an immune response to an antigen (Ag). The method comprises infecting
 CC target cells in the animal with recombinant alphavirus particles (AVP)
 CC that direct expression of at least one Ag, optionally modified, in the
 CC infected cells. AVP are derived from an alphavirus packaging cell line
 CC comprising a stably transformed expression cassette (EC) which expresses
 CC an alphavirus structural protein that is able, after introduction of an
 CC alphavirus vector construct (AVC), to produce recombinant AVP or the
 CC AVPs are free from recombinant AVPs that can initiate productive
 CC infection to produce infectious AVPs. The method is used, in human or
 CC veterinary medicine, to induce an immune response, particularly
 CC cell-mediated or HLA (human leucocyte antigen) Class I or II restricted,
 CC e.g. against viruses (especially hepatitis C), tumours, bacteria,
 CC parasites or fungi. Cells infected with alphavirus particles are fully
 CC viable and present antigens efficiently; the antigenic epitopes exposed
 CC can be altered by selective cloning of gene subfragments (including
 CC expression of multiple epitopes), and they effectively stimulate
 CC cytotoxic T cells. AA292892 to AA293018 and AA293017 represent sequences
 CC used in the exemplification of the present invention.
 XX Sequence 48 BP; 10 A; 2 C; 4 G; 32 T; 0 other;
 SQ

RESULT 47

AAZ59252/C
 XX ID AAZ59252 standard; DNA; 52 BP.
 XX AC AAZ59252;
 XX 06-SEP-1999 (first entry)
 XX Primer 4B used SIN-1 cDNA PCR.
 XX SIN-1; alphavirus; vector; infection; cancer; autoimmune disease;
 KW gene therapy; vaccine; primer; PCR; ss.
 XX Synthetic.
 OS Sindsbis virus.
 OS WO9738087-A2.
 XX 16-OCT-1997.
 XX 04-APR-1997; 97WO-US06010.
 XX 12-JUL-1996; 96US-0679640.
 PR 05-APR-1996; 96US-0628594.
 PR 24-JUN-1996; 96US-0668953.
 XX (CHIR) CHIRON VIAGENE INC.
 PA (UNIW) UNIV WASHINGTON.
 XX Belli BA, Dryga SA, Dubensky TW, Frolov I, Polo JM;
 PI Schlesinger S;
 PI WPI; 1997-512707/47.
 DR Nucleic acid comprising altered alpha-virus non-structural protein
 PT gene - useful for generating expression cassettes for production of
 PT recombinant proteins in vertebrate or insect cells
 XX Example 1; Page 99; 309pp; English.
 XX This primer oligonucleotide, termed 4B, includes an XbaI site, a
 CC T35 sequence, and nucleotides 11703-11698 of the Sindsbis virus
 CC genome. It was used in the PCR amplification of SIN-1 cDNA. A set
 CC of primer pairs necessary for amplifying the entire SIN-1 genome is
 CC provided (see AAZ59241-52). SIN-1 (see AAZ59321) is a Sindsbis virus
 CC variant strain which exhibits reduced inhibition of host
 CC macromolecular synthesis and which is capable of establishing
 CC persistent infection in vertebrate cells, in contrast to lytic,
 CC cytopathogenic wild-type strains of the same virus. The invention
 CC relates to alphavirus-based vectors with reduced inhibition of
 CC cellular macromolecular synthesis. Alphavirus vector constructs,
 CC replicons and eukaryotic layered vector initiation systems are used:
 CC (i) to deliver a selected heterologous sequence, particularly in
 CC gene therapy for treatment of a wide range of infections, cancers,
 CC and autoimmune diseases, or to regulate the immune system; (ii) as
 CC vaccines; (iii) to inhibit pathogenic; and (iv) to express
 CC heterologous products (therapeutic proteins, ribozymes, and
 CC antisense sequences). Since the modified vectors do not cause
 CC significant inhibition of host cell biosynthesis, they can be used
 CC safely as gene therapy vectors.
 XX Sequence 52 BP; 7 A; 1 C; 3 G; 41 T; 0 other;
 SQ

RESULT 48

AA58494/c
ID AAX58494 standard; DNA; 52 BP.

XX AC AAX58494;
XX

DT 16-AUG-1999 (first entry)

DE DE Primer 4B used SIN-1 cDNA PCR.

XX SIN-1; alphavirus; vector; infection; cancer; autoimmune disease;
KW gene therapy; vaccine; primer; PCR; ss.

XX OS Synthetic.
XX Sindbis virus.

XX WO9918226-A2.

XX PD 15-APR-1999.

XX PF 06-OCT-1998; 98WO-US21062.

XX PR 06-OCT-1997; 97US-0944465.

XX PA (CHIR) CHIRON CORP.
(UNIW) UNIV WASHINGTON.

XX PI Belli BA, Dryga SA, Dubensky TW, Frolov I, Polo JM;
PI Schlesinger S;

XX WPI; 1999-264032/22.

XX Alphavirus vectors with reduced cytopathic effects

XX Example 1; Page 103; 235pp; English.

XX This primer oligonucleotide, termed 4B, includes an XbaI site, a
T35 sequence, and nucleotides 11703-11698 of the Sindbis virus
genome. It was used in the PCR amplification of SIN-1 cDNA. A set
of primer pairs necessary for amplifying the entire SIN-1 genome is
provided (see AAX58483-94). SIN-1 (see AAX58571) is a Sindbis virus
variant strain which exhibits reduced inhibition of host
macromolecular synthesis and which is capable of establishing
persistent infection in vertebrate cells, in contrast to lytic,
cytopathogenic wild-type strains of the same virus. The invention
relates to alphavirus-based vectors with reduced inhibition of
cellular macromolecular synthesis. Alphavirus vector constructs,
replicons and eukaryotic layered vector initiation systems are used:
(i) to deliver a selected heterologous sequence, particularly in
gene therapy for treatment of a wide range of infections, cancers,
and autoimmune diseases, or to regulate the immune system; (ii) as
vaccines; (iii) to inhibit pathogens; and (iv) to express
heterologous products (therapeutic proteins, ribozymes, and
antisense sequences). Since the modified vectors do not cause
significant inhibition of host cell biosynthesis, they can be used
safely as gene therapy vectors.

XX Sequence 52 BP; 7 A; 1 C; 3 G; 41 T; 0 other;

XX Query Match 2.0%; Score 23; DB 20; Length 52;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaaa 1173
|||||

DB 51 ATTTCACAAAAA 29

RESULT 49
AAX59240/c

ID AAX59240 standard; DNA; 58 BP.

XX AC AAX59240;

XX

DT 06-SEP-1999 (first entry)

XX DE Primer 11,703R used in cDNA synthesis from SIN-1 RNA.

XX KW SIN-1; alphavirus; vector; infection; cancer; autoimmune disease;
KW gene therapy; vaccine; primer; ss.

XX OS Synthetic.
XX Sindbis virus.

XX PN WO9738087-A2.

XX PD 16-OCT-1997.

XX PF 04-APR-1997; 97WO-US06010.

XX PR 12-JUL-1996; 96US-0679640.

XX PR 05-APR-1996; 96US-0628594.

XX PR 24-JUN-1996; 96US-0668953.

XX PA (CHIR) CHIRON VIAGENE INC.
(UNIW) UNIV WASHINGTON.

XX PI Belli BA, Dryga SA, Dubensky TW, Frolov I, Polo JM;
PI Schlesinger S;

XX WPI; 1997-512707/47.

XX Nucleic acid comprising altered alpha-virus non-structural protein
gene - useful for generating expression cassettes for production of
recombinant proteins in vertebrate or insect cells

XX Example 1; Page 96; 309pp; English.

XX This primer oligonucleotide, termed 11,703R, includes an XhoI site,
a dt21 sequence, and nucleotides 11703-11677 of the Sindbis virus
genome. It was used in the preparation of first-strand cDNA from
genomic RNA isolated from SIN-1 virions. SIN-1 (see AAX59321) is a
Sindbis virus variant strain which exhibits reduced inhibition of
host macromolecular synthesis and which is capable of establishing
persistent infection in vertebrate cells, in contrast to lytic,
cytopathogenic wild-type strains of the same virus. The invention
relates to alphavirus-based vectors with reduced inhibition of
cellular macromolecular synthesis. Alphavirus vector constructs,
replicons and eukaryotic layered vector initiation systems are used:
(i) to deliver a selected heterologous sequence, particularly in
gene therapy for treatment of a wide range of infections, cancers,
and autoimmune diseases, or to regulate the immune system; (ii) as
vaccines; (iii) to inhibit pathogens; and (iv) to express
heterologous products (therapeutic proteins, ribozymes, and
antisense sequences). Since the modified vectors do not cause
significant inhibition of host cell biosynthesis, they can be used
safely as gene therapy vectors.

XX Sequence 58 BP; 13 A; 6 C; 8 G; 31 T; 0 other;

XX Query Match 2.0%; Score 23; DB 18; Length 58;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaaa 1173
|||||

DB 37 ATTTCACAAAAA 15

RESULT 50
AAX58482/c

ID AAX58482 standard; DNA; 58 BP.

XX AC AAX58482;

DT 16-AUG-1999 (first entry)
 XX Primer 11,703R used in cDNA synthesis from SIN-1 RNA.
 DE
 XX
 XX SIN-1; alphavirus; vector; infection; cancer; autoimmune disease;
 KW gene therapy; vaccine; primer; ss.
 XX
 XX Synthetic.
 OS Sindbis virus.
 XX
 XX WO9918226-A2.
 PN
 XX
 XX 15-APR-1999.
 PD
 XX
 XX 06-OCT-1998; 98WO-US21062.
 XX
 XX 06-OCT-1997; 97US-0944465.
 PR
 XX (CHIR) CHIRON CORP.
 PA (UNIW) UNIV WASHINGTON.
 XX
 XX Belli BA, Dryga SA, Dubensky TW, Frolov I, Polo JM;
 PI Schlesinger S;
 PI
 XX WPI; 1999-264032/22.
 DR
 XX
 XX Alphavirus vectors with reduced cytopathic effects
 PT
 XX
 XX Example 1; Page 100; 235pp; English.
 PS
 XX
 XX This primer oligonucleotide, termed 11,703R, includes an XhoI site,
 CC a dt21 sequence, and nucleotides 11703-11677 of the Sindbis virus
 CC genome. It was used in the preparation of first-strand cDNA from
 CC genomic RNA isolated from SIN-1 virions. SIN-1 (see AAX58571) is a
 CC Sindbis virus variant strain which exhibits reduced inhibition of
 CC host macromolecular synthesis and which is capable of establishing
 CC persistent infection in vertebrate cells, in contrast to lytic,
 CC cytopathogenic wild-type strains of the same virus. The invention
 CC relates to alphavirus-based vectors with reduced inhibition of
 CC cellular macromolecular synthesis. Alphavirus vector constructs,
 CC replicons and eukaryotic layered vector initiation systems are used:
 CC (i) to deliver a selected heterologous sequence, particularly in
 CC gene therapy for treatment of a wide range of infections, cancers,
 CC and autoimmune diseases, or to regulate the immune system; (ii) as
 CC vaccines; (iii) to inhibit pathogens; and (iv) to express
 CC heterologous products (therapeutic proteins, ribozymes, and
 CC antisense sequences). Since the modified vectors do not cause
 CC significant inhibition of host cell biosynthesis, they can be used
 CC safely as gene therapy vectors.
 XX
 XX Sequence 58 BP; 13 A; 6 C; 8 G; 31 T; 0 other;

Query Match 2.0%; Score 23; DB 20; Length 58;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1151 atttcaaaaaaaaaaaaaaa 1173
 Db 37 ATTTCAAAAAAAAAAAAAAAAA 15

Search completed: December 27, 2001, 15:20:28
 Job time: 1880 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 27, 2001, 14:49:08 ; Search time 1541.4 Seconds
(without alignments)
8177.500 Million cell updates/sec

Title: US-09-435-054-1
Perfect score: 1173
Sequence: 1 ccacgcgtccgccaccacac.....tcaaaaaaaaaaaaaaaaaa 1173

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 11351937 seqs, 5372889281 residues

Word size : 10

Total number of hits satisfying chosen parameters: 7889432

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

EST.*

1: em_estfun.*
2: em_esthum.*
3: em_estin.*
4: em_estom.*
5: em_estom.*
6: em_estba.*
7: em_estro.*
8: em_estov.*
9: em_estc.*
10: gb_esti.*
11: gb_est2.*
12: gb_hic.*
13: gb_gss.*
14: em_gss_fun.*
15: em_gss_hum.*
16: em_gss_inv.*
17: em_gss_pln.*
18: em_gss_pro.*
19: em_gss_rod.*
20: em_gss_vrt.*
21: em_gss_other.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	7.2	528	10	BE603222 HVSMH010
2	77	6.6	695	10	AU088581
3	47	4.0	594	10	AL506199 AL506199
4	38	3.2	441	10	AL509098
5	35	3.0	292	11	C28028
6	35	3.0	328	11	C19737
7	27	2.3	368	10	AW670176
8	27	2.3	387	11	BF042068
9	27	2.3	644	10	AV385922
10	26	2.2	67	11	BF013366
11	26	2.2	152	11	BI268661
12	26	2.2	153	11	BG379246

13	26	2.2	177	10	AW356324
14	26	2.2	304	11	BG733593
15	26	2.2	341	11	BG735487
16	26	2.2	342	11	BG603362
17	26	2.2	359	10	AI800247
18	26	2.2	361	11	BG625968
19	26	2.2	379	11	BF419334
20	26	2.2	384	11	BG652352
21	26	2.2	458	10	AW692142
22	26	2.2	458	10	AW790703
23	26	2.2	458	10	AW790704
24	26	2.2	464	11	BI312519
25	26	2.2	469	10	AL385635
26	26	2.2	472	10	AL380618
27	26	2.2	476	11	BI297090
28	26	2.2	488	10	AI302809
29	26	2.2	490	10	AI588492
30	26	2.2	510	10	AL382797
31	26	2.2	513	10	AI974955
32	26	2.2	530	10	AW066395
33	26	2.2	546	10	AW700042
34	26	2.2	554	10	AW067352
35	26	2.2	584	10	AI450987
36	26	2.2	618	11	BF646151
37	26	2.2	623	13	AZ369897
38	26	2.2	641	11	BF294174
39	26	2.2	683	11	BI094602
40	26	2.2	718	10	AW331967
41	26	2.2	794	10	AW331951
42	25	2.1	100	11	BG151615
43	25	2.1	151	10	AI348819
44	25	2.1	162	10	BE162370
45	25	2.1	174	10	AW424467
46	25	2.1	181	11	BE955607
47	25	2.1	202	10	AL377517
48	25	2.1	218	10	BE760641
49	25	2.1	248	10	AL383797
50	25	2.1	249	11	BG894227
51	25	2.1	275	10	AI619202
52	25	2.1	278	11	BF397037
53	25	2.1	279	11	BG628355
54	25	2.1	280	11	W91845
55	25	2.1	284	10	AI972310
56	25	2.1	286	11	Z21519
57	25	2.1	288	11	BG249632
58	25	2.1	296	11	BG183578
59	25	2.1	300	11	BF301972
60	25	2.1	313	10	AI965374
61	25	2.1	314	10	AA426259
62	25	2.1	316	10	AW620622
63	25	2.1	320	10	AW632871
64	25	2.1	343	11	BF273439
65	25	2.1	344	10	BE193387
66	25	2.1	344	10	BE318043
67	25	2.1	347	10	AW747449
68	25	2.1	348	10	AI288430
69	25	2.1	350	10	AI204600
70	25	2.1	360	10	AI592230
71	25	2.1	380	10	AV189558
72	25	2.1	383	10	AA901378
73	25	2.1	385	10	AI059972
74	25	2.1	386	11	BG046412
75	25	2.1	392	10	AI301010
76	25	2.1	392	10	AI452746
77	25	2.1	396	10	AI302775
78	25	2.1	397	11	H88112
79	25	2.1	403	11	BI401262
80	25	2.1	405	11	BG373364
81	25	2.1	408	10	AI087244
82	25	2.1	410	11	BG444160
83	25	2.1	417	10	AW589142
84	25	2.1	420	10	AI619296
85	25	2.1	424	10	AA812319

c 86	25	2.1	425	10	AI623732	ts38f03.x	c 159	24	2.0	108	10	AA169635	AA169635	zo94h07.s
c 87	25	2.1	431	11	BG377948	UI-R-CX00-	c 160	24	2.0	148	10	BE014640	BE014640	126444 MA
c 88	25	2.1	431	11	BI294121	UI-R-DKO-	c 161	24	2.0	172	10	BF522452	BF522452	UI-R-C3-U
c 89	25	2.1	432	11	BF277163	GA_EB002	c 162	24	2.0	173	11	BI284278	BI284278	UI-R-CX09
c 90	25	2.1	433	10	AA879981	VW02f08.f	c 163	24	2.0	176	11	BG349623	BG349623	947031F03
c 91	25	2.1	433	10	AA271535	VB72f06.f	c 164	24	2.0	184	11	BF396055	BF396055	UI-R-B52-
c 92	25	2.1	434	10	AW333719	S25B11 AG	c 165	24	2.0	191	10	AI030368	AI030368	UI-R-C0-J
c 93	25	2.1	435	10	AW761531	s168g10.y	c 166	24	2.0	194	10	AU031968	AU031968	AU031968
c 94	25	2.1	436	10	AW196592	XM35B08.x	c 167	24	2.0	195	10	AI619140	AI619140	486086A01
c 95	25	2.1	438	10	AI682080	tp46g07.x	c 168	24	2.0	208	11	BG942050	BG942050	ax20e05.x
c 96	25	2.1	444	10	BE123824	JAYB0070.	c 169	24	2.0	216	10	AL040259	AL040259	DKE2d434J
c 97	25	2.1	447	10	AW160132	JAYNOA16.	c 170	24	2.0	217	10	AI678285	AI678285	tu86a12.x
c 98	25	2.1	448	10	AI112054	UI-R-YO-m	c 171	24	2.0	217	10	AI885110	AI885110	w189n02.x
c 99	25	2.1	450	11	BG023267	q39b06.x	c 172	24	2.0	224	10	AI873168	AI873168	wf47e01.x
c 100	25	2.1	451	11	BI347841	q648h01.x	c 173	24	2.0	231	10	AW148355	AW148355	xf13e06.x
c 101	25	2.1	454	11	BI295424	UI-R-DKO-	c 174	24	2.0	240	10	AW026780	AW026780	vv44h08.x
c 102	25	2.1	457	13	AQ224364	HS_225B_B	c 175	24	2.0	242	11	BF458765	BF458765	UI-N-B21-
c 103	25	2.1	459	10	AU100788	AU100788	c 176	24	2.0	248	10	AI696390	AI696390	tw60e10.x
c 104	25	2.1	460	11	BF712183	MI-P-E6-a	c 177	24	2.0	251	10	AL386827	AL386827	MCBC37B02
c 105	25	2.1	461	10	AF051125	AF051125	c 178	24	2.0	251	10	AA297325	AA297325	EST112861
c 106	25	2.1	463	11	BG874056	MEST45-G1	c 179	24	2.0	253	10	AW423296	AW423296	sh65g05.y
c 107	25	2.1	466	10	AU077751	AU077751	c 180	24	2.0	255	10	AW458259	AW458259	sh80d10.y
c 108	25	2.1	466	11	BF408506	UI-R-BJ2-	c 181	24	2.0	264	11	BF389206	BF389206	UI-R-B52-
c 109	25	2.1	470	10	AW585203	N211477e	c 182	24	2.0	267	10	AW173411	AW173411	98f07ne.f
c 110	25	2.1	472	10	AL381858	MCBC03D08	c 183	24	2.0	276	10	AV240460	AV240460	AV240460
c 111	25	2.1	472	10	AT001659	AT001659	c 184	24	2.0	276	11	BF870582	BF870582	IL3-ET011
c 112	25	2.1	477	11	BF464809	UI-M-CG0P	c 185	24	2.0	279	10	AL512111	AL512111	AL512111
c 113	25	2.1	482	11	BF889899	289509 MA	c 186	24	2.0	285	11	BF458810	BF458810	UI-M-B21-
c 114	25	2.1	488	10	AL373094	MCBA55F02	c 187	24	2.0	289	10	AA838181	AA838181	oe11f02.s
c 115	25	2.1	494	10	AL501779	AL501779	c 188	24	2.0	290	10	AI274624	AI274624	qv11f08.x
c 116	25	2.1	494	11	BF072624	NCSM3F8T7	c 189	24	2.0	291	11	BE945090	BE945090	UI-M-B21-
c 117	25	2.1	500	10	AI514014	GH27054.3	c 190	24	2.0	291	11	BE991925	BE991925	UI-M-B21-
c 118	25	2.1	510	10	AL385151	MCBC26F09	c 191	24	2.0	292	11	C90944	C90944	C90944
c 119	25	2.1	512	10	AI751483	cn10c03.y	c 192	24	2.0	293	10	AI641518	AI641518	fc16g01.x
c 120	25	2.1	514	10	AV539740	AV539740	c 193	24	2.0	303	10	AW253664	AW253664	UI-R-BJ0-
c 121	25	2.1	518	10	AW505123	UI-HF-BN0	c 194	24	2.0	307	10	AW657453	AW657453	110669 MA
c 122	25	2.1	523	10	AI739789	606051B09	c 195	24	2.0	314	10	AI844207	AI844207	UI-M-AL1-
c 123	25	2.1	526	11	BG023036	daa82908.	c 196	24	2.0	315	10	AW489528	AW489528	UI-M-BH3-
c 124	25	2.1	531	10	AI559017	AEMTBA39	c 197	24	2.0	320	10	AI713661	AI713661	UI-R-AG1-
c 125	25	2.1	535	10	AI884559	wn34c03.x	c 198	24	2.0	322	10	AW291523	AW291523	UI-M-B12-
c 126	25	2.1	537	10	AW332367	S7E8 AGS-	c 199	24	2.0	323	10	AW457172	AW457172	UI-M-BH3-
c 127	25	2.1	540	10	AL501793	AL501793	c 200	24	2.0	329	10	AL381507	AL381507	MCBC01D07
c 128	25	2.1	551	10	AA46329	zw67G02.s	c 201	24	2.0	330	10	AL381506	AL381506	MCBC01D07
c 129	25	2.1	554	13	BH004117	BMBAC07H1	c 202	24	2.0	333	11	BG631069	BG631069	CC-esf1cl
c 130	25	2.1	558	11	BF644533	NF014H04E	c 203	24	2.0	334	10	AI548133	AI548133	UI-R-C3-S
c 131	25	2.1	563	10	AW463485	BP230012B	c 204	24	2.0	334	10	AW522236	AW522236	UI-R-B00-
c 132	25	2.1	564	10	BF639131	946021C02	c 205	24	2.0	334	10	BE103651	BE103651	UI-R-BX0-
c 133	25	2.1	571	10	AL499965	AL499965	c 206	24	2.0	335	11	R79241	R79241	y188g03.sl
c 134	25	2.1	575	11	BI285870	UI-R-CX0s	c 207	24	2.0	339	10	AI511107	AI511107	UI-R-BT0-
c 135	25	2.1	578	11	C99725	C99725 Rice	c 208	24	2.0	339	10	AW458897	AW458897	sh16c08.y
c 136	25	2.1	581	10	AA986450	uel13d05.x	c 209	24	2.0	340	11	BE993341	BE993341	UI-M-B21-
c 137	25	2.1	608	11	BG300891	HVSMEX001	c 210	24	2.0	341	11	BG058181	BG058181	nah21g05.
c 138	25	2.1	610	10	AU030234	AU030234	c 211	24	2.0	341	11	BF603618	BF603618	269175 MA
c 139	25	2.1	613	10	AW965505	EST377593	c 212	24	2.0	342	11	R49579	R49579	y968f10.sl
c 140	25	2.1	614	10	AW139756	UI-H-B11-	c 213	24	2.0	347	13	AZ427469	AZ427469	1M0209L24
c 141	25	2.1	637	11	BG414824	HVSMEX000	c 214	24	2.0	348	10	AI373517	AI373517	qz46f04.x
c 142	25	2.1	639	11	BG415609	HVSMEX000	c 215	24	2.0	348	10	AA190776	AA190776	zp88g01.s
c 143	25	2.1	648	11	BG378168	UI-R-CV1-	c 216	24	2.0	350	10	AU031081	AU031081	AU031081
c 144	25	2.1	668	10	AA218943	zr02h04.s	c 217	24	2.0	353	10	AV661109	AV661109	AV661109
c 145	25	2.1	668	13	AQ508212	RPCI-11-2	c 218	24	2.0	358	10	AA523352	AA523352	n167b05.s
c 146	25	2.1	671	10	AL510350	AL510350	c 219	24	2.0	367	10	AA708908	AA708908	z164a05.s
c 147	25	2.1	698	13	B28405	F18G11TF IG	c 220	24	2.0	369	10	BE097533	BE097533	UI-R-B01-
c 148	25	2.1	706	11	BI284433	COBAU0020	c 221	24	2.0	374	11	BI042730	BI042730	CM4-OT016
c 149	25	2.1	715	10	AI055045	COBAU0020	c 222	24	2.0	375	10	AI087166	AI087166	oz59f11.x
c 150	25	2.1	746	11	BF107484	601823816	c 223	24	2.0	377	10	AU101345	AU101345	AU101345
c 151	25	2.1	769	10	BE033408	ME01C01 M	c 224	24	2.0	377	11	BG631702	BG631702	CC-esf1cl
c 152	25	2.1	770	10	AV402769	AV402769	c 225	24	2.0	379	11	BF457952	BF457952	UI-M-B21-
c 153	25	2.1	785	11	BF275540	GA_E5002	c 226	24	2.0	383	11	BG939706	BG939706	cr60h12.x
c 154	25	2.1	791	13	AQ892327	HS_3100_B	c 227	24	2.0	384	11	BE097913	BE097913	UI-R-BX0-
c 155	25	2.1	799	13	AQ898961	HS_3131_A	c 228	24	2.0	385	11	BG939871	BG939871	ax01f10.y
c 156	25	2.1	808	13	BO31105	CSRL-167H7-	c 229	24	2.0	386	10	AA528468	AA528468	ne99g07.s
c 157	25	2.1	868	11	BG418528	HVSMEX001	c 230	24	2.0	387	10	AU092049	AU092049	AU092049
c 158	24	2.0	91	10	AI590755	tw18d10.x	c 231	24	2.0	387	10	BE035723	BE035723	MO10A02 M

C 232	24	2.0	388	10	AA960665	UB60D12.S	305	24	2.0	481	10	AA708500	AA708500
C 233	24	2.0	388	11	BG627170	CC-ESF1CL	306	24	2.0	481	10	AA708500	AA708500
C 234	24	2.0	389	10	AW197753	CC-ESF1CL	307	24	2.0	482	11	AA708500	AA708500
C 235	24	2.0	391	10	AI394151	W60F04.X	C 307	24	2.0	482	13	AA708500	AA708500
C 236	24	2.0	391	10	AI394151	W60F04.X	308	24	2.0	483	13	AA708500	AA708500
C 237	24	2.0	392	11	BI294681	UI-R-AGI-	309	24	2.0	483	13	AA708500	AA708500
C 238	24	2.0	393	10	AI360437	WY9C09.X	310	24	2.0	486	13	AA708500	AA708500
C 239	24	2.0	393	10	AI360437	WY9C09.X	311	24	2.0	486	13	AA708500	AA708500
C 240	24	2.0	393	10	AI360437	WY9C09.X	312	24	2.0	492	10	AA708500	AA708500
C 241	24	2.0	393	11	BG734784	CC-ESF1CL	313	24	2.0	493	10	AA708500	AA708500
C 242	24	2.0	394	10	AI705697	UI-R-ADP1-	314	24	2.0	493	11	AA708500	AA708500
C 243	24	2.0	395	10	AI705697	UI-R-ADP1-	315	24	2.0	497	13	AA708500	AA708500
C 244	24	2.0	397	11	AI705697	UI-R-ADP1-	316	24	2.0	498	11	AA708500	AA708500
C 245	24	2.0	399	10	BG626898	CC-ESF1CL	C 317	24	2.0	499	10	AA708500	AA708500
C 246	24	2.0	399	10	AI752996	CC-ESF1CL	318	24	2.0	500	10	AA708500	AA708500
C 247	24	2.0	406	11	AI845108	UI-M-BG0-	319	24	2.0	502	10	AA708500	AA708500
C 248	24	2.0	406	11	AI845108	UI-M-BG0-	320	24	2.0	506	10	AA708500	AA708500
C 249	24	2.0	407	10	AI843568	UI-M-AO1-	321	24	2.0	506	10	AA708500	AA708500
C 250	24	2.0	407	10	AI843568	UI-M-AO1-	322	24	2.0	506	10	AA708500	AA708500
C 251	24	2.0	407	11	H68635	WY9C09.X	323	24	2.0	509	11	AA708500	AA708500
C 252	24	2.0	408	11	BF462451	UI-M-CG0P	324	24	2.0	510	10	AA708500	AA708500
C 253	24	2.0	408	11	BF462451	UI-M-CG0P	325	24	2.0	512	11	AA708500	AA708500
C 254	24	2.0	409	11	AI953784	W60F04.X	326	24	2.0	514	11	AA708500	AA708500
C 255	24	2.0	409	11	AI953784	W60F04.X	327	24	2.0	514	11	AA708500	AA708500
C 256	24	2.0	413	11	BI417043	CC-ESF1CL	328	24	2.0	515	11	AA708500	AA708500
C 257	24	2.0	417	10	AI102123	UI-M-BG0-	329	24	2.0	517	11	AA708500	AA708500
C 258	24	2.0	417	10	AI102123	UI-M-BG0-	330	24	2.0	518	10	AA708500	AA708500
C 259	24	2.0	420	11	BG825045	UI-M-BG0-	331	24	2.0	521	10	AA708500	AA708500
C 260	24	2.0	421	10	AI002637	UI-M-BG0-	332	24	2.0	522	10	AA708500	AA708500
C 261	24	2.0	424	10	AA965089	UI-M-BG0-	333	24	2.0	526	11	AA708500	AA708500
C 262	24	2.0	425	10	BE578812	UI-M-BG0-	334	24	2.0	528	11	AA708500	AA708500
C 263	24	2.0	426	10	AI079526	WY9C09.X	335	24	2.0	528	13	AA708500	AA708500
C 264	24	2.0	428	10	AA766113	W60F04.X	336	24	2.0	530	10	AA708500	AA708500
C 265	24	2.0	428	10	AA766113	W60F04.X	337	24	2.0	530	10	AA708500	AA708500
C 266	24	2.0	428	11	BI302732	UI-M-BG0-	338	24	2.0	531	10	AA708500	AA708500
C 267	24	2.0	428	11	BI302732	UI-M-BG0-	339	24	2.0	534	10	AA708500	AA708500
C 268	24	2.0	428	11	BI302732	UI-M-BG0-	340	24	2.0	534	10	AA708500	AA708500
C 269	24	2.0	431	10	AI548796	UI-M-BG0-	341	24	2.0	536	10	AA708500	AA708500
C 270	24	2.0	431	10	AI548796	UI-M-BG0-	342	24	2.0	536	10	AA708500	AA708500
C 271	24	2.0	432	11	BG371896	UI-M-BG0-	343	24	2.0	540	10	AA708500	AA708500
C 272	24	2.0	432	11	BG371896	UI-M-BG0-	344	24	2.0	541	10	AA708500	AA708500
C 273	24	2.0	432	11	BG371896	UI-M-BG0-	345	24	2.0	542	10	AA708500	AA708500
C 274	24	2.0	441	10	AW298453	UI-M-BG0-	346	24	2.0	542	10	AA708500	AA708500
C 275	24	2.0	442	10	AW298453	UI-M-BG0-	347	24	2.0	543	11	AA708500	AA708500
C 276	24	2.0	443	10	AW492587	UI-M-BG0-	348	24	2.0	543	11	AA708500	AA708500
C 277	24	2.0	443	11	H05676	WY9C09.X	349	24	2.0	544	10	AA708500	AA708500
C 278	24	2.0	448	11	BF457871	UI-M-BG0-	350	24	2.0	546	10	AA708500	AA708500
C 279	24	2.0	448	10	AA977956	UI-M-BG0-	351	24	2.0	547	11	AA708500	AA708500
C 280	24	2.0	453	10	AI741264	WY9C09.X	352	24	2.0	547	11	AA708500	AA708500
C 281	24	2.0	454	10	AW252481	UI-M-BG0-	353	24	2.0	550	10	AA708500	AA708500
C 282	24	2.0	455	10	AW252481	UI-M-BG0-	354	24	2.0	550	10	AA708500	AA708500
C 283	24	2.0	455	10	AW252481	UI-M-BG0-	355	24	2.0	551	11	AA708500	AA708500
C 284	24	2.0	457	10	AW2529026	UI-M-BG0-	356	24	2.0	551	11	AA708500	AA708500
C 285	24	2.0	458	10	AW2529026	UI-M-BG0-	357	24	2.0	554	11	AA708500	AA708500
C 286	24	2.0	459	11	BF703305	UI-M-BG0-	358	24	2.0	562	11	AA708500	AA708500
C 287	24	2.0	459	13	AQ218977	HS-2009.A	359	24	2.0	564	11	AA708500	AA708500
C 288	24	2.0	460	10	AI739036	WY9C09.X	360	24	2.0	565	10	AA708500	AA708500
C 289	24	2.0	460	10	AI739036	WY9C09.X	361	24	2.0	566	10	AA708500	AA708500
C 290	24	2.0	462	10	AI031947	UI-M-BG0-	362	24	2.0	566	11	AA708500	AA708500
C 291	24	2.0	463	10	AI031947	UI-M-BG0-	363	24	2.0	566	11	AA708500	AA708500
C 292	24	2.0	466	10	AI057265	WY9C09.X	364	24	2.0	571	10	AA708500	AA708500
C 293	24	2.0	468	10	AI738431	WY9C09.X	365	24	2.0	573	11	AA708500	AA708500
C 294	24	2.0	471	10	AA748606	WY9C09.X	366	24	2.0	577	10	AA708500	AA708500
C 295	24	2.0	472	11	BF419501	UI-M-BG0-	367	24	2.0	577	10	AA708500	AA708500
C 296	24	2.0	473	10	AW734152	UI-M-BG0-	368	24	2.0	578	10	AA708500	AA708500
C 297	24	2.0	473	10	BE108673	UI-M-BG0-	369	24	2.0	582	11	AA708500	AA708500
C 298	24	2.0	474	10	AW731994	WY9C09.X	370	24	2.0	584	11	AA708500	AA708500
C 299	24	2.0	474	10	AW731994	WY9C09.X	371	24	2.0	586	11	AA708500	AA708500
C 300	24	2.0	474	10	AW731994	WY9C09.X	372	24	2.0	587	11	AA708500	AA708500
C 301	24	2.0	478	10	AI558276	WY9C09.X	373	24	2.0	589	10	AA708500	AA708500
C 302	24	2.0	478	10	BE46185	WY9C09.X	374	24	2.0	590	10	AA708500	AA708500
C 303	24	2.0	479	10	BE350119	WY9C09.X	375	24	2.0	592	13	AA708500	AA708500
C 304	24	2.0	480	10	AA190481	WY9C09.X	376	24	2.0	599	11	AA708500	AA708500
							377	24	2.0	601	10	AA708500	AA708500

C 378	24	2.0	605	10	AL501906	AL501906	AL501906	C 451	23	2.0	140	10	AI467491
C 379	24	2.0	606	13	B6385	CIT-HSP-200	B6385 CIT-HSP-200	C 452	23	2.0	141	10	AW485611
C 380	24	2.0	612	11	BE948552	UI-M-BH3-	BE948552 UI-M-BH3-	C 453	23	2.0	143	11	BF059386
C 381	24	2.0	617	10	BE580934	kp83c10.y	BE580934 kp83c10.y	C 454	23	2.0	145	10	AU162554
C 382	24	2.0	617	13	BH005572	BMEAC09M2	BH005572 BMEAC09M2	C 455	23	2.0	146	11	BI300136
C 383	24	2.0	624	10	A1691878	wc80b04.x	A1691878 wc80b04.x	C 456	23	2.0	146	11	BF225185
C 384	24	2.0	624	10	A1691878	605011G09	A1691878 605011G09	C 457	23	2.0	151	10	AI348971
C 385	24	2.0	630	10	A1067182	ESW208854	A1067182 ESW208854	C 458	23	2.0	152	10	AI254067
C 386	24	2.0	633	10	AW173527	xj08c01.x	AW173527 xj08c01.x	C 459	23	2.0	152	10	BE155800
C 387	24	2.0	635	10	AV650924	AV650924	AV650924 AV650924	C 460	23	2.0	154	10	AW023605
C 388	24	2.0	636	10	AL596792	DKE2p451J	AL596792 DKE2p451J	C 461	23	2.0	156	11	EG940736
C 389	24	2.0	642	13	A2651906	IM0522P21	A2651906 IM0522P21	C 462	23	2.0	160	10	AA754333
C 390	24	2.0	646	13	AK334535	S36A11 AG	AK334535 S36A11 AG	C 463	23	2.0	162	11	EG058871
C 391	24	2.0	650	10	AV650865	AV650865	AV650865 AV650865	C 464	23	2.0	163	10	AW145795
C 392	24	2.0	655	10	AW162107	au73b07.x	AW162107 au73b07.x	C 465	23	2.0	166	10	AW155711
C 393	24	2.0	659	11	BI300991	UI-R-DK0-	BI300991 UI-R-DK0-	C 466	23	2.0	166	11	BF470457
C 394	24	2.0	660	10	AV650443	AV650443	AV650443 AV650443	C 467	23	2.0	168	11	EG316794
C 395	24	2.0	660	11	BG840808	MEST12-A1	BG840808 MEST12-A1	C 468	23	2.0	168	11	AI597856
C 396	24	2.0	668	10	AV711203	AV711203	AV711203 AV711203	C 469	23	2.0	169	10	AI043033
C 397	24	2.0	668	10	NM689417	NF019A03S	NM689417 NF019A03S	C 470	23	2.0	170	11	BI043033
C 398	24	2.0	671	13	A0404011	RPCI-23-3	A0404011 RPCI-23-3	C 471	23	2.0	172	11	EG630959
C 399	24	2.0	678	13	A0469180	CITBI-EI-	A0469180 CITBI-EI-	C 472	23	2.0	172	11	BF146549
C 400	24	2.0	682	10	AK334058	S29H1 AGS	AK334058 S29H1 AGS	C 473	23	2.0	172	11	BF146549
C 401	24	2.0	685	13	AQ308749	CITBI-EI-	AQ308749 CITBI-EI-	C 474	23	2.0	174	10	AI043033
C 402	24	2.0	691	10	AV650877	AV650877	AV650877 AV650877	C 475	23	2.0	174	10	AI0306203
C 403	24	2.0	708	10	AU097613	AU097613	AU097613 AU097613	C 476	23	2.0	174	11	BE17570
C 404	24	2.0	710	10	AK334145	S31A11 AG	AK334145 S31A11 AG	C 477	23	2.0	174	11	BF577945
C 405	24	2.0	715	13	AQ317030	CITBI-EI-	AQ317030 CITBI-EI-	C 478	23	2.0	174	11	EG005063
C 406	24	2.0	718	10	BE216256	BE216256 HV-CEB001	BE216256 HV-CEB001	C 479	23	2.0	176	13	AZ432866
C 407	24	2.0	719	11	C97610	C97610 C97610 Rice	C97610 C97610 Rice	C 480	23	2.0	177	11	EG509243
C 408	24	2.0	740	11	BI284285	BI284285 UI-R-CX0S	BI284285 UI-R-CX0S	C 481	23	2.0	179	11	BF12174
C 409	24	2.0	761	11	BF466933	UI-M-CG0P	BF466933 UI-M-CG0P	C 482	23	2.0	180	13	AQ467828
C 410	24	2.0	766	10	AV652860	AV652860	AV652860 AV652860	C 483	23	2.0	180	13	AI010512
C 411	24	2.0	771	10	AK331991	S1E8 AGS-	AK331991 S1E8 AGS-	C 484	23	2.0	183	10	AI010512
C 412	24	2.0	798	13	CNS06N08	AL407238 T7 end of	AL407238 T7 end of	C 485	23	2.0	183	10	AI270013
C 413	24	2.0	801	13	AQ308510	CITBI-EI-	AQ308510 CITBI-EI-	C 486	23	2.0	183	11	BF704134
C 414	24	2.0	809	10	BE564064	BE564064 601348024	BE564064 601348024	C 487	23	2.0	184	10	BE049135
C 415	24	2.0	851	13	AQ750504	HS-5576.B	AQ750504 HS-5576.B	C 488	23	2.0	186	11	EG606807
C 416	24	2.0	877	11	BF663790	602145226	BF663790 602145226	C 489	23	2.0	189	11	EG156808
C 417	24	2.0	885	11	BF065790	BF065790 HV-CEB001	BF065790 HV-CEB001	C 490	23	2.0	191	10	AI824801
C 418	24	2.0	1104	10	AU167403	AU167403	AU167403 AU167403	C 491	23	2.0	193	10	AL512088
C 419	24	2.0	1369	10	BE421655	BE421655 HWM012CD.	BE421655 HWM012CD.	C 492	23	2.0	193	11	EG509721
C 420	24	2.0	1579	12	AK014727	AK014727 Mus muscu	AK014727 Mus muscu	C 493	23	2.0	196	10	AI445580
C 421	24	2.0	2481	12	BC011742	BC011742 Homo sapi	BC011742 Homo sapi	C 494	23	2.0	197	11	BI135038
C 422	24	2.0	2608	12	AF119843	AF119843 Homo sapi	AF119843 Homo sapi	C 495	23	2.0	198	11	BI042969
C 423	23	2.0	36	10	AW059764	AW059764 LE4C03.Yq	AW059764 LE4C03.Yq	C 496	23	2.0	199	10	AA598553
C 424	23	2.0	60	10	AW409793	AW409793 fh02d08.Y	AW409793 fh02d08.Y	C 497	23	2.0	200	10	BE216903
C 425	23	2.0	63	10	AI340465	AI340465 tq24c11.x	AI340465 tq24c11.x	C 498	23	2.0	200	10	BE216903
C 426	23	2.0	75	10	AW698623	AW698623 g538 glan	AW698623 g538 glan	C 499	23	2.0	200	10	BE573993
C 427	23	2.0	76	11	BI151596	BI151596 nag61h07.	BI151596 nag61h07.	C 500	23	2.0	200	11	BI268745
C 428	23	2.0	90	10	AI246927	AI246927 qx72q02.x	AI246927 qx72q02.x	C 501	23	2.0	200	11	BF408107
C 429	23	2.0	95	10	AI565331	AI565331 t173b06.x	AI565331 t173b06.x	C 502	23	2.0	201	10	BF414859
C 430	23	2.0	98	11	BF579653	BF579653 602093529	BF579653 602093529	C 503	23	2.0	201	10	AI149954
C 431	23	2.0	99	11	BF579266	BF579266 602093437	BF579266 602093437	C 504	23	2.0	205	11	EG630646
C 432	23	2.0	106	10	AA529379	AA529379 v139e11.r	AA529379 v139e11.r	C 505	23	2.0	205	11	F05641
C 433	23	2.0	107	11	BG894048	BG894048 kt17e01.Y	BG894048 kt17e01.Y	C 506	23	2.0	206	11	BF990241
C 434	23	2.0	107	11	BF571999	BF571999 nai61e03.	BF571999 nai61e03.	C 507	23	2.0	208	11	BF411099
C 435	23	2.0	108	11	BF580150	BF580150 602099159	BF580150 602099159	C 508	23	2.0	209	10	AA432258
C 436	23	2.0	108	11	BG236561	BG236561 nai45c04.	BG236561 nai45c04.	C 509	23	2.0	212	10	AI91817
C 437	23	2.0	116	11	R26750	R26750 yH44a05.S1	R26750 yH44a05.S1	C 510	23	2.0	214	10	AI036797
C 438	23	2.0	117	10	AI289791	AI289791 qw12c03.x	AI289791 qw12c03.x	C 511	23	2.0	214	10	AI818231
C 439	23	2.0	130	10	AW690406	AW690406 NF032G12S	AW690406 NF032G12S	C 512	23	2.0	214	10	AI825612
C 440	23	2.0	120	11	BF467777	BF467777 UI-M-CG0-	BF467777 UI-M-CG0-	C 513	23	2.0	215	10	AL380992
C 441	23	2.0	121	11	BG090795	BG090795 mac10c04.	BG090795 mac10c04.	C 514	23	2.0	217	10	AI649758
C 442	23	2.0	122	10	AI655445	AI655445 ts98g11.x	AI655445 ts98g11.x	C 515	23	2.0	217	10	AW414918
C 443	23	2.0	122	10	AL047559	AL047559 DKE2p586E	AL047559 DKE2p586E	C 516	23	2.0	217	11	EG456558
C 444	23	2.0	123	10	AI447232	AI447232 mq97h01.x	AI447232 mq97h01.x	C 517	23	2.0	218	11	AL0442529
C 445	23	2.0	127	10	AU161810	AU161810 AU161810	AU161810 AU161810	C 518	23	2.0	218	11	BF044007
C 446	23	2.0	129	10	AW074332	AW074332 xbl1c01.x	AW074332 xbl1c01.x	C 519	23	2.0	219	11	AW156260
C 447	23	2.0	132	10	AW396329	AW396329 sh03b12.Y	AW396329 sh03b12.Y	C 520	23	2.0	219	11	BI248615
C 448	23	2.0	132	10	AW495627	AW495627 UI-M-BH3-	AW495627 UI-M-BH3-	C 521	23	2.0	220	10	AW237005
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C 450	23	2.0	138	10	AW151446	AW151446 xg27a03.x	AW151446 xg27a03.x	C 523	23	2.0	221	11	BF465396

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C 674	23	2.0	313	10	AI430964	AI430964 m145f01.x	747	23	2.0	347	10	AI889943	AI889943 wm65e01.x
C 675	23	2.0	313	10	BE024072	BE024072 sm96d01.y	748	23	2.0	347	10	AI182023	AI182023 AU182023
C 676	23	2.0	314	11	BE996624	BE996624 UI-M-BZ1-	749	23	2.0	347	11	BG630213	BG630213 CC-esf1cL
C 677	23	2.0	314	11	BG377624	BG377624 UI-R-CU0-	750	23	2.0	348	10	AI045405	AI045405 UI-R-Cl-k
C 678	23	2.0	315	10	AA676604	AA676604 ad38h09.s	751	23	2.0	349	10	AI467100	AI467100 vd65a07.x
C 679	23	2.0	315	10	AI350489	AI350489 qe17g02.x	752	23	2.0	349	10	AL384430	AL384430 MIBC22A08
C 680	23	2.0	316	10	AW101900	AW101900 AU101900	753	23	2.0	350	10	AU031357	AU031357 AU031357
C 681	23	2.0	316	11	BE808365	BE808365 213641.MA	754	23	2.0	351	11	BG628565	BG628565 CC-esf1cL
C 682	23	2.0	318	10	AA731127	AA731127 nw68f01.s	755	23	2.0	352	10	AW090822	AW090822 xc94c09.x
C 683	23	2.0	318	13	AAQ474700	AAQ474700 C1TBI-E1-	756	23	2.0	352	10	AW691766	AW691766 FST34H09S
C 684	23	2.0	319	10	AA761084	AA761084 nyl13f10.s	757	23	2.0	352	10	AW959823	AW959823 EOT371894
C 685	23	2.0	319	10	AI921915	AI921915 wm86e12.x	758	23	2.0	354	10	AI853058	AI853058 UI-M-BHO-
C 686	23	2.0	319	11	BI013908	BI013908 BM3-EF020	759	23	2.0	354	10	AU034731	AU034731 AU034731
C 687	23	2.0	320	10	AI463087	AI463087 u881h01.x	760	23	2.0	354	11	BF541814	BF541814 602068486
C 688	23	2.0	320	10	AW407392	AW407392 UI-HF-BM0	761	23	2.0	355	10	AA766825	AA766825 oa39g05.s
C 689	23	2.0	320	11	BI297803	BI297803 UI-R-CV2-	762	23	2.0	355	10	AW016443	AW016443 UI-H-B10p
C 690	23	2.0	322	10	AA733187	AA733187 z978g05.s	763	23	2.0	355	10	AW058281	AW058281 wx18c05.x
C 691	23	2.0	322	10	AW503799	AW503799 UI-HF-BN0	764	23	2.0	355	11	BI300076	BI300076 UI-R-CV2-
C 692	23	2.0	322	10	BE584713	BE584713 5-5E-Z0.P	765	23	2.0	355	11	BF418401	BF418401 UI-R-BJ2-
C 693	23	2.0	322	11	BF270221	BF270221 GA_EB000	766	23	2.0	356	10	AW339279	AW339279 xz89g06.x
C 694	23	2.0	323	10	AI383565	AI383565 tc45e08.x	767	23	2.0	356	10	BE553897	BE553897 ur44a02.x
C 695	23	2.0	323	10	AU066075	AU066075 AU066075	768	23	2.0	357	11	BI300059	BI300059 UI-R-CV2-
C 696	23	2.0	323	11	BI276625	BI276625 UI-R-CX0-	769	23	2.0	357	11	T98458	T98458 ye60h01.r1
C 697	23	2.0	324	10	AI400047	AI400047 tg90e04.x	770	23	2.0	358	10	AU032431	AU032431 AU032431
C 698	23	2.0	324	10	AU164885	AU164885 AU164885	771	23	2.0	358	11	T83606	T83606 yd64c03.r1
C 699	23	2.0	325	10	AW278284	AW278284 sf42b04.y	772	23	2.0	358	11	BE946474	BE946474 UI-M-B20-
C 700	23	2.0	325	11	BG943273	BG943273 ax35f08.x	773	23	2.0	359	10	AI620691	AI620691 tu85g08.x
C 701	23	2.0	326	11	BI298061	BI298061 UI-R-CV2-	774	23	2.0	360	10	AI873669	AI873669 wm28c02.x
C 702	23	2.0	327	10	AI454550	AI454550 UI-R-BT0-	775	23	2.0	361	10	AI835429	AI835429 UI-M-AQ0-
C 703	23	2.0	327	10	AA534248	AA534248 nj70g01.s	776	23	2.0	362	10	AL377097	AL377097 MIB29D002
C 704	23	2.0	327	11	BI135017	BI135017 UI-M-BH3-	777	23	2.0	362	10	AW152186	AW152186 xf75h04.x
C 705	23	2.0	328	10	AI449664	AI449664 mf52g03.x	778	23	2.0	362	10	BE439176	BE439176 CDO1335.W
C 706	23	2.0	328	11	BG056762	BG056762 naf9g10.	779	23	2.0	362	11	BI297407	BI297407 UI-R-CV2-
C 707	23	2.0	329	10	AA279091	AA279091 z882d03.s	780	23	2.0	363	13	AQ590764	AQ590764 HS-2104.A
C 708	23	2.0	329	11	BF521936	BF521936 UI-R-C2p-	781	23	2.0	364	10	AW761212	AW761212 nz20c03.s
C 709	23	2.0	330	10	AI853332	AI853332 UI-M-BH0-	782	23	2.0	364	10	AI821603	AI821603 nc47d01.x
C 710	23	2.0	331	10	AW169224	AW169224 x120f08.x	783	23	2.0	364	10	AU089779	AU089779 AU089779
C 711	23	2.0	332	10	AU101705	AU101705 AU101705	784	23	2.0	364	10	AU069375	AU069375 cr45a07.x
C 712	23	2.0	333	10	AI547552	AI547552 UI-R-C3-s	785	23	2.0	364	11	W78770	W78770 zh49e12.r1
C 713	23	2.0	333	10	AW630479	AW630479 hh83b12.y	786	23	2.0	365	10	AA984877	AA984877 am62c09.s
C 714	23	2.0	334	10	AA729900	AA729900 nx40c08.s	787	23	2.0	365	10	AI791842	AI791842 nc47d01.y
C 715	23	2.0	335	10	A1224417	A1224417 qx11g05.x	788	23	2.0	365	10	AW081385	AW081385 xc41f09.x
C 716	23	2.0	335	10	AI659538	AI659538 tul2b05.x	789	23	2.0	366	10	AA528443	AA528443 ne84d07.s
C 717	23	2.0	335	10	AI843698	AI843698 UI-M-AL1-	790	23	2.0	366	11	BG629901	BG629901 CC-esf1cL
C 718	23	2.0	335	10	AA512593	AA512593 vj19a07.r	791	23	2.0	366	11	BE969598	BE969598 601679728
C 719	23	2.0	336	10	AL376831	AL376831 MEBB26F04	792	23	2.0	367	10	AI304451	AI304451 qc54a05.x
C 720	23	2.0	336	11	BF416379	BF416379 UI-R-CA0-	793	23	2.0	368	10	AW072923	AW072923 xa38b12.x
C 721	23	2.0	337	10	AA956755	AA956755 UI-R-E1-f	794	23	2.0	369	13	AZ754678	AZ754678 cq02f10.f
C 722	23	2.0	337	10	AI214729	AI214729 q967c12.x	795	23	2.0	370	10	AW170669	AW170669 xi85g05.x
C 723	23	2.0	337	10	AU031985	AU031985 AU031985	796	23	2.0	370	11	BG378423	BG378423 UI-R-CU0-
C 724	23	2.0	337	11	BG627186	BG627186 CC-esf1cL	797	23	2.0	370	11	C96639	C96639 C96639 R1ce
C 725	23	2.0	337	11	BF458322	BF458322 UI-M-BZ1-	798	23	2.0	371	10	AI117892	AI117892 uc39g03.r
C 726	23	2.0	338	11	BI288594	BI288594 UI-R-DK0-	799	23	2.0	371	10	AI359680	AI359680 gy33h01.x
C 727	23	2.0	338	11	BE993303	BE993303 UI-M-BZ1-	800	23	2.0	371	10	AL368169	AL368169 MCB22F05
C 728	23	2.0	339	10	AA725247	AA725247 al16b09.s	801	23	2.0	371	10	AW456371	AW456371 UI-M-BH3-
C 729	23	2.0	340	10	AW020544	AW020544 df11c10.y	802	23	2.0	371	10	AW950359	AW950359 EST362429
C 730	23	2.0	340	10	AW085718	AW085718 xb43c08.x	803	23	2.0	371	11	BG626209	BG626209 CC-esf1cL
C 731	23	2.0	340	11	W74730	W74730 zd56a07.s1	804	23	2.0	371	11	BG812173	BG812173 daf6h005.
C 732	23	2.0	340	11	BF272776	BF272776 GA_EB001	805	23	2.0	372	10	AA748404	AA748404 oa56b12.s
C 733	23	2.0	341	10	AV695430	AV695430 UI-R-ET1-	806	23	2.0	372	10	AW792139	AW792139 DO1026-R
C 734	23	2.0	341	10	AW529323	AW529323 UI-R-ET1-	807	23	2.0	372	10	AI690720	AI690720 tx88e05.x
C 735	23	2.0	341	11	BF272535	BF272535 GA_EB001	808	23	2.0	373	10	AI690720	AI690720 tx88e05.x
C 736	23	2.0	341	11	BF462684	BF462684 UI-M-CG0p	809	23	2.0	373	10	BE057180	BE057180 sm97f06.y
C 737	23	2.0	342	10	AV742957	AV742957 AV742957	810	23	2.0	373	11	BG372191	BG372191 UI-R-CV0-
C 738	23	2.0	343	10	AW044671	AW044671 w774a06.x	811	23	2.0	373	11	H00246	H00246 yj22a11.r1
C 739	23	2.0	343	10	AW634283	AW634283 bl18g06.w	812	23	2.0	374	11	BF408154	BF408154 UI-R-BJ2-
C 740	23	2.0	344	10	BE116785	BE116785 UI-R-B81-	813	23	2.0	374	10	BF465582	BF465582 UI-M-CG0p
C 741	23	2.0	345	10	BE663032	BE663032 105724.MA	814	23	2.0	375	10	AU161967	AU161967 AU161967
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C 818	23	2.0	377	10	AI201315	qf71c04.x	C 891	23	2.0	404	10	AW069880	AW069880 cr52g12.x
C 819	23	2.0	378	10	AW584377	CTT-HSP-2	C 892	23	2.0	404	10	AA425874	AA425874 zv47c09.s
C 820	23	2.0	378	13	AQ021775	CTT-HSP-2	C 893	23	2.0	405	10	AI511149	AI511149 UI-R-BT0-
C 821	23	2.0	379	11	BG455899	NF070807P	C 894	23	2.0	405	10	AW311516	AW311516 sg40q10.y
C 822	23	2.0	380	10	AW620714	s108f10.y	C 895	23	2.0	405	11	BI297551	BI297551 UI-R-CV2-
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C 826	23	2.0	381	11	BI293258	UI-R-DK0-	C 899	23	2.0	406	10	AW562937	AW562937 660070A01
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C 829	23	2.0	382	11	BG381530	UI-R-CT0-	C 902	23	2.0	406	11	BI304203	BI304203 UI-R-DK0-
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C 832	23	2.0	382	11	BG091454	mac15e10.	C 905	23	2.0	407	10	AI366180	AI366180 MTA05D12
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C 840	23	2.0	386	10	AW516950	xq05a01.x	C 913	23	2.0	410	10	AI753436	AI753436 cr10e08.x
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C 842	23	2.0	388	10	AW457668	UI-W-BH3-	C 915	23	2.0	411	10	AI763551	AI763551 UI-R-Y0-a
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C 846	23	2.0	391	10	AI024618	ov52f11.x	C 919	23	2.0	412	11	BG374749	BG374749 UI-R-CV1-
C 847	23	2.0	391	10	AI077575	oz33h08.x	C 920	23	2.0	412	11	BG378496	BG378496 UI-R-CU0-
C 848	23	2.0	391	11	BE990739	UI-M-BZ1-	C 921	23	2.0	413	11	BG627918	BG627918 CC-esf1cL
C 849	23	2.0	391	11	BF984054	602306996	C 922	23	2.0	413	11	BI302772	BI302772 UI-R-DK0-
C 850	23	2.0	392	10	AA979748	MEST1-C12	C 923	23	2.0	414	10	AA425118	AA425118 zv47c09.r
C 851	23	2.0	392	11	BI298590	CTT-HSP-556	C 924	23	2.0	414	11	BF373833	BF373833 MI-P-AV1-
C 852	23	2.0	392	13	B78988	CTT-HSP-556	C 925	23	2.0	414	11	BF712341	BF712341 MI-P-A3-a
C 853	23	2.0	393	10	AI1593392	q047g09.x	C 926	23	2.0	414	11	BG194478	BG194478 RSL13637
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C 860	23	2.0	395	10	AA911813	ok74f10.s	C 933	23	2.0	416	11	BG079525	BG079525 H3041D12-
C 861	23	2.0	395	10	AA763191	BP230011B	C 934	23	2.0	417	10	BE350903	BE350903 hc3f05.x
C 862	23	2.0	396	10	AA757248	ah69c03.s	C 935	23	2.0	417	10	AA748850	AA748850 ny77a08.s
C 863	23	2.0	396	11	BE996131	UI-M-BZ1-	C 936	23	2.0	418	10	AA835741	AA835741 od66g04.s
C 864	23	2.0	397	10	AI737578	T110056e	C 937	23	2.0	418	10	AI395196	AI395196 MA002612.x
C 865	23	2.0	397	10	AW576599	UI-HF-BR0	C 938	23	2.0	418	10	AL373107	AL373107 MTA55F09
C 866	23	2.0	398	10	AI016996	ou2a08.x	C 939	23	2.0	418	11	T92195	T92195 yel17f09.s1
C 867	23	2.0	398	10	AL383634	MEBC15F05	C 940	23	2.0	418	11	BF410994	BF410994 UI-R-CN0-
C 868	23	2.0	398	10	AA265303	mu66g04.r	C 941	23	2.0	419	10	AA859622	AA859622 UI-R-E0-b
C 869	23	2.0	398	10	BE669477	7el3d02.x	C 942	23	2.0	419	10	AW152559	AW152559 xf76c11.x
C 870	23	2.0	398	11	BF465302	UI-M-CG0p	C 943	23	2.0	419	10	AW664138	AW664138 hi04g12.x
C 871	23	2.0	398	11	BG272299	nab87a07	C 944	23	2.0	419	11	BG670871	BG670871 DRNEHC09
C 872	23	2.0	400	10	AI335623	qt24e01.x	C 945	23	2.0	419	11	BI297368	BI297368 UI-R-CV2-
C 873	23	2.0	400	10	AL373268	MEBA56G09	C 946	23	2.0	419	11	C97095	C97095 C97095 Rice
C 874	23	2.0	400	10	AW152441	xg64f06.x	C 947	23	2.0	420	10	AI571916	AI571916 tr71b10.x
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C 877	23	2.0	401	11	BG438944	de71f12.x	C 950	23	2.0	420	11	BG656930	BG656930 df37f01.y
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C 879	23	2.0	401	11	BE994286	UI-M-CG0p	C 952	23	2.0	421	10	AL512003	AL512003 AL512003
C 880	23	2.0	401	11	BG042207	su93b01.y	C 953	23	2.0	421	11	BI059437	BI059437 IL3-UT011
C 881	23	2.0	402	10	RA037708	zk37d07.s	C 954	23	2.0	422	10	AW599486	AW599486 qa87a02.y
C 882	23	2.0	402	10	AI753714	cr14b07.x	C 955	23	2.0	422	11	BG155431	BG155431 sab4a11.
C 883	23	2.0	403	10	AI126202	q086f05.x	C 956	23	2.0	423	11	BI403015	BI403015 MI-P-CF1-
C 884	23	2.0	403	10	AI339816	qk68f10.x	C 957	23	2.0	424	11	BG633062	BG633062 GH19443.5
C 885	23	2.0	403	10	AI983521	w233b10.x	C 958	23	2.0	424	11	BI298212	BI298212 UI-R-CV2-
C 886	23	2.0	403	10	AW151977	xf71b11.x	C 959	23	2.0	425	10	AL376844	AL376844 MTA55F09
C 887	23	2.0	403	10	AW491800	UI-M-BH3-	C 960	23	2.0	425	10	BE638807	BE638807 946014C08
C 888	23	2.0	403	11	BG631320	CC-esf1cL	C 961	23	2.0	425	11	BI298733	BI298733 UI-R-CV2-


```

305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@br.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/.

FEATURES
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Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 375 tgggcatgagcgcctcgcttcgactacgt 409
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Db 128 TGGCCATGAGCGCGCTCGCTTCGAGCTACGT 162

RESULT 6
LOCUS C19737 328 bp mRNA EST 24-OCT-1996
DEFINITION C19737 Rice panicle at ripening stage Oryza sativa cDNA clone
ACCESSION E10861_1A, mRNA sequence.
VERSION C19737.1 GI:1632008
KEYWORDS EST.
SOURCE Oryza sativa.
  ORGANISM
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    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzoideae; Oryza.
REFERENCE
  AUTHORS
    Sasaki, T.
  TITLE
    Rice cDNA from panicle at ripening stage
  JOURNAL
    Unpublished (1996)
  COMMENT
    Contact: Takuji Sasaki
    National Institute of Agrobiological Resources
    Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
    305-8602, Japan
    Tel: 81-298-38-7441
    Fax: 81-298-38-7468
    Email: tsasaki@br.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/.

FEATURES
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 18;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 189 ctgatgccgctcggaacgtgctccgcatcgcg 223
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Db 101 CTGATGCCGATCGGACGTCGATCGCATCGC 135

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Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@br.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/.

FEATURES
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Best Local Similarity 100.0%; Pred. No. 18;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 101 CTGATGCCGATCGGACGTCGATCGCATCGC 135

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RESULT 7
LOCUS AW670176 368 bp mRNA EST 25-APR-2001
DEFINITION 114040 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION AW670176
VERSION AW670176.1 GI:7526690
KEYWORDS EST.
SOURCE COW.
  ORGANISM
    Bos taurus
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
    Bovidae; Bovinae; Bos.
REFERENCE
  AUTHORS
    1 (bases 1 to 368)
    Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
    Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S., Bennett,
    G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
    Perlea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
    Keele, J.W.
  TITLE
    Sequence evaluation of four pooled-tissue normalized bovine cDNA
    libraries and construction of a gene index for cattle
  JOURNAL
    Genome Res. 11 (4), 626-630 (2001)
  COMMENT
    Contact: Smith TPL
    USDA, ARS, US Meat Animal Research Center
    PO Box 166, Clay Center, NE 68933-0166, USA
    Tel: 402 762 4366
    Fax: 402 762 4390
    Email: smith@email.marc.usda.gov
    Single pass sequencing. Bases called and alt_trimmed with phred
    v0.980904.e. Vector identified by cross_match with the -minscore 18
    and -minmatch 12 options.
    PCR Primers
    FORWARD: AGGAACAGCTATGACCAT
    BACKWARD: GTTTCCTCAGTCACGACG
    Plate: 111 row: M column: 16
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BASE COUNT 130 a 44 c 75 g 119 t
ORIGIN

Query Match 2.3%; Score 27; DB 10; Length 368;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1147 gattatttcaaaaaaaaaaaaaaaaaa 1173
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Db 249 GATATTTCACAAAAAATAAAAAA 275

RESULT 8
LOCUS BF042068 387 bp mRNA EST 10-OCT-2000
DEFINITION BP250013A20D7 Soares normalized bovine placenta Bos taurus cDNA
clone BP250013A20D7 5', mRNA sequence.
ACCESSION BF042068
VERSION BF042068.1 GI:10759195
KEYWORDS EST.
SOURCE COW.
  ORGANISM
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    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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    Bovidae; Bovinae; Bos.
REFERENCE
  1 (bases 1 to 387)

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AUTHORS Lewin, H.A., Soares, M.B., Rebeiz, M., Pardinas, J., Liu, L. and Larson, J.H.

TITLE Bovine ESTs

JOURNAL Unpublished (2000)

COMMENT Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu

Funding for cattle EST sequencing was provided by the USDA National Research Initiative, Animal Genome Resource Grant AG 99-3205-8534 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Center. Vector Trimmer g: Cross_match from Washington University Genome Center PHRAP suite. This sequence is vector free and at least 200 bp in length. REPEAT IN THE SEQUENCE Simple_repeat STRAND (+) ELEMENT (A)n LOCATION [365, 386].

PCR Primers
FORWARD: TAATACGACTCACTATAGGG
BACKWARD: ATTACCTCTCACTAAG
Insert Length: 387 Std Error: 0.00
Plate: BP250013A20 row: D column: 7
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High quality sequence stop: 387.

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Location/Qualifiers
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/note="Organ: placenta; Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI; The cDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806."

BASE COUNT 149 a 66 c 65 g 107 t

ORIGIN

Query Match 2.3%; Score 27; DB 11; Length 387;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1147 gattattcaaaaaaaaaaaaaaaaaa 1173
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Db 356 GATTATTTCAAAAAAAAAAAAAAAAA 382

RESULT 9
AV385922 644 bp mRNA EST 27-OCT-1999
LOCUS AV385922 Halocynthia roretzi Fertilized egg Halocynthia roretzi
DEFINITION cDNA clone 007G18_3 3', mRNA sequence.
ACCESSION AV385922
VERSION AV385922.1 GI:6130979
KEYWORDS EST.
SOURCE Halocynthia roretzi.
ORGANISM Halocynthia roretzi.
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Halocynthia.
1 (bases 1 to 644)
Makabe, K.W.
Halocynthia roretzi EST
Unpublished (1999)
Contact: Kazuhiro W. Makabe
Department of Zoology, Graduate School of Science
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan

ECORI. The library was constructed by Dr. Andrew Kloek at Divergence LLC and Brandi Chiapelli and Dr. James McCarter at Washington University, St. Louis. Nematodes were provided by Dr. David Bird of North Carolina State University."

BASE COUNT 26 a 17 c 3 g 21 t
ORIGIN

Query Match 2.2%; Score 26; DB 11; Length 67;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1148 attatttcaaaaaa 1173
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Db 10 ATTATTTCAAAAAA 35

RESULT 11
BI268661
LOCUS 152 bp mRNA EST 18-JUL-2001
DEFINITION NF015H10GS1F1091 Germinating Seed Medicago truncatula cDNA clone
ACCESSION NF015H10GS 5', mRNA sequence.
VERSION BI268661
KEYWORDS EST.
SOURCE GI:14874736
ORGANISM barrel medic.
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

REFERENCE 1 (bases 1 to 152)
AUTHORS Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula germinating seed library
JOURNAL Unpublished (2001)
COMMENT Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 152 Std Error: 0.00
Plate: 015 row: H column: 10
Seq primer: TCACACAGGAACAGCTATGAC.

FEATURES
Location/Qualifiers
1..152

/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF015H10GS"
/clone_lib="Germinating Seed"
/tissue_type="germinating seeds"
/dev_stage="0, 1, 2 and 3 days after acid treatment."
/note="Vector: Lambda Zap; M. truncatula seeds were acid treated and placed on wet filter papers in petri dishes. Seeds were harvested at 0, 1, 2 and 3 days after acid treatment. cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from each time point. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-Zap XR vector using ExAssist helper phage and the E. coli strain XL1-Blue MRF' (Stratagene).
Excised plasmids were plated using SOLR cells."

BASE COUNT 70 a 24 c 16 g 42 t
ORIGIN

Query Match 2.2%; Score 26; DB 11; Length 152;

Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1148 attatttcaaaaaa 1173
|||||
Db 120 ATTATTTCAAAAAA 145

RESULT 12
BG379246/c
LOCUS 153 bp mRNA EST 12-MAR-2001
DEFINITION BG379246
UI-R-BT1-bnn-c-04-0-UI.s1 UI-R-BT1 Rattus norvegicus cDNA clone
UI-R-BT1-bnn-c-04-0-UI 3', mRNA sequence.

ACCESSION BG379246
VERSION BG379246.1 GI:13303718
KEYWORDS EST.
SOURCE Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 153)
AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized corpus-striatum library cDNA Library preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 1-27,
>AT_rich_low_complexity
Seq primer: M13 Forward
POLYA=Yes.

FEATURES
Location/Qualifiers

1..153
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-BT1-bnn-c-04-0-UI"
/clone_lib="UI-R-BT1"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The library UI-R-BT1 is a subtracted library derived from a mixture of the following tissues: hippocampus, thalamus, mid-brain, medulla, corpus striatum, cerebral cortex and testis. For a detailed description of the library from which this clone was derived, please visit our web site at rattus.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_LIB=UI-R-BT1
TAG_TISSUE=corpus-striatum
TAG_SEQ=CTAGG"

BASE COUNT 32 a 29 c 37 g 55 t
ORIGIN

Query Match 2.2%; Score 26; DB 11; Length 153;

```

Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaaaaaaaaaaaaaa 1173
    |||||||
Db 26 ATTATTTCACAAAAAAAAAAAAAAAAA 1

RESULT 13
ACCESSION AW356324 177 bp mRNA EST 25-APR-2001
LOCUS 38607 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
DEFINITION AW356324
ACCESSION AW356324
VERSION AW356324.1 GI:5860330
KEYWORDS EST.
SOURCE COW.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 177)
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
Perteau,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
Keele,J.W.
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
JOURNAL Genome Res. 11 (4), 626-630 (2001)
MEDLINE 21180013
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smitht@mail.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCCAGTCACGACG
Plate: 19 row: F column: 14
Seq primer: ATTAGTGACACTATAG.
FEATURES
    Location/Qualifiers
    1..177
    /Organism="Bos taurus"
    /db_xref="taxon:9913"
    /clone_lib="MARC 2BOV"
    /tissue_type="pooled"
    /lab_host="DH108"
    /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
    Library made from pooled tissue from testis, thymus,
    semitendinosus muscle, longissimus muscle, pancreas,
    adrenal, and endometrium."
BASE COUNT 62 a 22 c 17 g 76 t
ORIGIN

Query Match 2.2%; Score 26; DB 10; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaaaaaaaaaaaaaa 1173
    |||||||
Db 151 ATTATTTCACAAAAAAAAAAAAAAAAA 176

RESULT 14
ACCESSION BG735393 304 bp mRNA EST 15-MAY-2001
LOCUS CC-escfLEL7F07d1 Tomato flower library from a mixture of
DEFINITION developmental stages Lycopersicon esculentum cDNA, mRNA sequence.

```

```

ACCESSION BG735393
VERSION BG735393.1 GI:14085082
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 304)
AUTHORS van der Hoeven,R.S. and Tanksley,S.D.
TITLE ESTs from a tomato flower library
JOURNAL Unpublished (2001)
COMMENT Contact: Rutgers S. van der Hoeven
Cornell University
252 Emerson Hall, Ithaca, NY 14850, USA
Tel: 607 255 7886
Fax: 607 255 6683
Email: rv19@cornell.edu
3 prime sequence.
FEATURES
    Location/Qualifiers
    1..304
    /Organism="Lycopersicon esculentum"
    /cultivar="56203"
    /db_xref="taxon:4081"
    /clone_lib="tomato flower library from a mixture of
    developmental stages"
    /tissue_type="developing flower buds and open flowers"
    /dev_stage="4-8 week old plants"
    /lab_host="XLOLR"
    /note="Vector: pBK_CMV; Site_1: EcoRI; Site_2: XhoI;
    Flowers and flower buds were collected from greenhouse
    grown plants and used for library construction (cLEL)."
BASE COUNT 122 a 48 c 40 g 94 t
ORIGIN

Query Match 2.2%; Score 26; DB 11; Length 304;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaaaaaaaaaaaaaa 1173
    |||||||
Db 26 ATTATTTCACAAAAAAAAAAAAAAAAA 1

RESULT 15
ACCESSION BG735487/c 341 bp mRNA EST 15-MAY-2001
LOCUS CC-escfLEL8J20d1 Tomato flower library from a mixture of
DEFINITION developmental stages Lycopersicon esculentum cDNA, mRNA sequence.
ACCESSION BG735487
VERSION BG735487.1 GI:14085176
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 341)
AUTHORS van der Hoeven,R.S. and Tanksley,S.D.
TITLE ESTs from a tomato flower library
JOURNAL Unpublished (2001)
COMMENT Contact: Rutgers S. van der Hoeven
Cornell University
252 Emerson Hall, Ithaca, NY 14850, USA
Tel: 607 255 7886
Fax: 607 255 6683
Email: rv19@cornell.edu
3 prime sequence.
FEATURES
    Location/Qualifiers
    1..341

```

```

/organism="Lycopersicon esculentum"
/cultivar="F6203"
/db_xref="taxon:4081"
/clone_lib="tomato flower library from a mixture of
developmental stages"
/tissue_type="developing flower buds and open flowers"
/dev_stage="4-8 week old plants"
/lab_host="XLOLR"
/notes="Vector: pBK_CMV; Site_1: EcoRI; Site_2: XhoI;
Flowers and flower buds were collected from greenhouse
grown plants and used for library construction (cLEL)."
"
BASE COUNT      98 a   58 c   56 g   129 t
ORIGIN

Query Match      2.2%; Score 26; DB 11; Length 341;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaaaaaaaaaaaaa 1173
|||||
Db 26 ATTATTTCACAAAAAAAAAAAAAAAAA 1

RESULT 16
BG603362      342 bp   mRNA      EST      14-AUG-2001
LOCUS
DEFINITION EST502452 Plasmodium yoelii sporozoite cDNA Plasmodium yoelii cDNA
clone PYCDQ79, mRNA sequence.
ACCESSION BG603362
VERSION
KEYWORDS
SOURCE
ORGANISM Plasmodium yoelii.
REFERENCE 1 (bases 1 to 342)
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
Kappe,S.H.I., Gardner,M.J., Brown,S.M., Ross,J., Matuschewski,K.,
Ribeiro,J.M., Adams,J.H., Quackenbush,J., Cho,J., Carucci,D.J.,
Hoffman,S.L. and Nussenzweig,V.
Exploring the transcriptome of the malaria sporozoite stage
Proc. Natl. Acad. Sci. U. S. A. 98 (17), 9895-9900 (2001)
Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org
Request for clones, please contact: Stefan Kappe,
kappes01@popmail.med.nyu.edu Michael Heidelberg Division,
Department of Pathology New York University School of Medicine.
FEATURES
source
Location/Qualifiers
1. .342
/organism="Plasmodium yoelii"
/strain="17XNL"
/db_xref="taxon:5861"
/clone="PYCDQ79"
/clone_lib="Plasmodium yoelii sporozoite cDNA"
/dev_stage="sporozoites from salivary gland"
/lab_host="E. coli TOP10"
/notes="Vector: pCR4; TA cloning; Plasmodium yoelii
sporozoite cDNA library from salivary gland sporozoites 14
days post-infection"
BASE COUNT      180 a   30 c   27 g   105 t
ORIGIN

Query Match      2.2%; Score 26; DB 11; Length 342;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaaaaaaaaaaaaa 1173
|||||

```

```

Db 265 ATTATTTCACAAAAAAAAAAAAAAAAA 290

RESULT 17
AI800247/c      359 bp   mRNA      EST      06-JUL-1999
LOCUS
DEFINITION t175a01.x1 NCI-CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2137800 3',
mRNA sequence.
ACCESSION AI800247
VERSION AI800247.1 GI:5365719
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 359)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -400P from Gibco.
Location/Qualifiers
1. .359
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2137800"
/clone_lib="NCI-CGAP_Kid11"
/lab_host="DH10B"
/notes="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI-CGAP_Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 132376-132391, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo."
BASE COUNT      125 a   68 c   39 g   127 t
ORIGIN

Query Match      2.2%; Score 26; DB 10; Length 359;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaaaaaaaaaaaaa 1173
|||||
Db 31 ATTATTTCACAAAAAAAAAAAAAAAAA 6

RESULT 18
BG625968/c      361 bp   mRNA      EST      19-APR-2001
LOCUS
DEFINITION cc-esf1cLEL10F17a1 Tomato flower library from a mixture of
developmental stages Lycopersicon esculentum cDNA clone
cc-esf1cLEL10F17a1, mRNA sequence.
ACCESSION BG625968
VERSION BG625968.1 GI:13677441
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;

```


Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 361)
van der Hoeven,R.S. and Tanksley,S.D.
ESTs from a tomato flower library
Unpublished (2001)
Contact: Rutgers S. van der Hoeven
Cornell University
252 Emerson Hall, Ithaca, NY 14850, USA
Tel: 607 255 7886
Fax: 607 255 6683
Email: rv19@cornell.edu

3 prime sequence.
Location/Qualifiers
1. 361
/organism="Lycopersicon esculentum"
/cultivar="E6203"
/db_xref="taxon:4081"
/clone="CC-esfLcLE110F17a1"
/clone_lib="tomato flower library from a mixture of developmental stages"
/tissue_type="developing flower buds and open flowers"
/dev_stage="4-8 week old plants"
/lab_host="XLOLR"
/note="Vector: PBK_CMV; Site_1: EcoRI; Site_2: XhoI; Flowers and flower buds were collected from greenhouse grown plants and used for library construction (cLEL)."
BASE COUNT 131 a 73 c 61 g 95 t 1 others
ORIGIN

Query Match 2.2%; Score 26; DB 11; Length 361;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaa 1173
|||||
DB 26 ATTATTTCAAAAA 1

RESULT 19
LOCUS BF419934/c 379 bp mRNA EST 28-NOV-2000
DEFINITION UI-R-BJ2-bph-h-10-0-UI.s1 UI-R-BJ2 Rattus norvegicus cDNA clone
UI-R-BJ2-bph-h-10-0-UI 3', mRNA sequence.
ACCESSION BF419934
VERSION BF419934.1 GI:11407923
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 379)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized heart library cDNA Library Preparation: M.B. Soares Lab

Clone distribution: clones will be available through Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=yes.

FEATURES
source
Location/Qualifiers
1. 379
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-BJ2-bph-h-10-0-UI"
/clone_lib="UI-R-BJ2"
/note="Vector: DH10B (Life Technologies)"
/note="Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BJ2 library is a subtracted library derived from the following tissues: heart, atrium at 15 dpc, ventricle at 16.5 dpc, atrium at 16.5 dpc, ventricle at 13 dpc, ventricle at 15 dpc, AV canal at 15 dpc. For a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_LIB=UI-R-BJ2
TAG_TISSUE=heart
TAG_SEQ=ACAAAC"
BASE COUNT 87 a 89 c 104 g 99 t
ORIGIN

Query Match 2.2%; Score 26; DB 11; Length 379;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaa 1173
|||||
DB 26 ATTATTTCAAAAA 1

RESULT 20
LOCUS BG652352/c 384 bp mRNA EST 25-APR-2001
DEFINITION sad65h07.y1 Gm-cl051 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-cl051-5342 5', mRNA sequence.
ACCESSION BG652352
VERSION BG652352.1 GI:13789761
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 384)
AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or info.genomesystems.com web site: www.genomesystems.com

```

Putative full length read
vector to vector length is 385.
FEATURES
  Source
    1..384
      /organism="Glycine max"
      /db_xref="taxon:3847"
      /clone="GENOME SYSTEMS CLONE ID: Gm-cl051-5342"
      /clone_lib="Gm-cl051"
      /tissue_type="floral meristematic mRNA"
      /lab_host="DH10B"
      /note="Vector: pluescript II SK+; Site_1: EcoRI; Site_2:
      XhoI; The cDNA library was constructed from floral
      meristematic mRNA provided by Dr. Halina Knap of Clemson
      University. Complementary DNA was synthesized from mRNA
      using a primer consisting of a poly(dT) sequence with a
      XhoI restriction site. EcoRI adapters were ligated to the
      blunt-ended cDNA fragments followed by XhoI digestion. The
      cDNA fragments were directionally cloned into the
      EcoRI-XhoI restriction site of the pBluescript vector. The
      ligated cDNA fragments were transformed into DH10B host
      cells (GibcoBRL). This library was constructed in the
      laboratory of Dr. Randy Shoemaker."
BASE COUNT      111 a      89 c      37 g      147 t
ORIGIN

Query Match      2.2%; Score 26; DB 11; Length 384;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 31 ATTATTTCACCAAAAAAAAAAAAAAAAAA 6

RESULT 21
AW692142/c
LOCUS
DEFINITION
  NF052F06ST1F1000 Developing stem Medicago truncatula cDNA clone
  NF052F06ST 5', mRNA sequence.
ACCESSION
  AW692142
VERSION
  AW692142.2 GI:11957103
KEYWORDS
  EST.
SOURCE
  Medicago truncatula
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
  Medicago.
REFERENCE
  1 (bases 1 to 458)
  He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
  ,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
  ,R.A.
  Expressed Sequence Tags from the Samuel Roberts Noble Foundation
  Medicago truncatula stem library
  Unpublished (2000)
  On Apr 14, 2000 this sequence version replaced gi:7566878.
  Contact: Dixon RA
  Plant Biology Division
  The Samuel Roberts Noble Foundation
  2510 Sam Noble Parkway, Ardmore, OK 73402, USA
  Tel: 580 221 7302
  Fax: 580 221 7380
  Email: radixon@noble.org
  Insert Length: 692 Std Error: 0.00
  Plate: 052 row: F column: 06
  Seq primer: TCACACAGGAAACAGCTATGAC.
FEATURES
  source
    1..458
      /organism="Medicago truncatula"
      /db_xref="taxon:3880"
      /clone="NF052F06ST"
      /clone_lib="Developing stem"

```

```

/tissue_type="stem"
/dev_stage="pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of
internodal stem segments"
BASE COUNT      146 a      82 c      77 g      153 t
ORIGIN

Query Match      2.2%; Score 26; DB 10; Length 458;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 52 ATTATTTCACCAAAAAAAAAAAAAAAAAA 27

RESULT 22
AW790703
LOCUS
DEFINITION
  D00136-F Lambda Zap, Stratagene Blumeria graminis f. sp. hordei
  cDNA clone D00136 similar to nadh-ubiquinone oxidoreductase 9.5 kd
  subun, mRNA sequence.
ACCESSION
  AW790703
VERSION
  AW790703.1 GI:13902300
KEYWORDS
  EST.
SOURCE
  Blumeria graminis f. sp. hordei.
  Blumeria graminis f. sp. hordei
  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
  Erysiphales; Erysiphaceae; Blumeria.
REFERENCE
  1 (bases 1 to 458)
  Thomas,S.W., Rasmussen,S.W., Glaring,M.A., Rouster,J.A. and Oliver
  ,R.P.
  Gene identification in the fungal pathogen Blumeria graminis by
  expressed sequence tag analysis
  Unpublished (2000)
  Contact: Rasmussen,S.W.
  Department of Yeast Genetics
  Carlsberg Laboratory
  10 GI. Carlsbergvej, DK-2500, Copenhagen, Denmark
  Tel: 45 3327 5230
  Fax: 45 3327 4766
  Email: sw@rcg.dk
  High quality sequence stop: 458
  POLYA=Yes.
FEATURES
  source
    1..458
      /organism="Blumeria graminis f. sp. hordei"
      /db_xref="taxon:62688"
      /clone="D00136"
      /clone_lib="Lambda Zap, Stratagene"
      /cell_type="conidia"
      /lab_host="Hordeum vulgare"
BASE COUNT      153 a      94 c      86 g      125 t
ORIGIN

Query Match      2.2%; Score 26; DB 10; Length 458;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 432 ATTATTTCACCAAAAAAAAAAAAAAAAAA 457

RESULT 23
AW790704
LOCUS
DEFINITION
  D00136-R Lambda Zap, Stratagene Blumeria graminis f. sp. hordei
  cDNA clone D00136 similar to nadh-ubiquinone oxidoreductase 9.5 kd
  subun, mRNA sequence.
ACCESSION
  AW790704

```


fungus Glomus intraradices (Schenck & Smith, isolate LPA8). The plants were watered every day and twice a week with a modified nutrient Long Ashton solution without phosphate but with a high level of nitrate. After 3 weeks RNA was extracted from whole root systems. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-zap XR vector from Stratagene and packaged using Gigapack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using ExAssit helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Sequençage (Genoscope, Evry, France). Note : EST may be of fungal origin."

BASE COUNT 154 a 70 c 81 g 164 t
ORIGIN

Query Match 2.2%; Score 26; DB 10; Length 469;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 435 ATTATTTCRAAAAAAAAAAAAAAAAAA 460

RESULT 26
LOCUS AI380618 472 bp mRNA EST 30-MAR-1999
DEFINITION tg02b08.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107575 3'
similar to gb:X62534 HIGH MOBILITY GROUP PROTEIN HMG2 (HUMAN
); Contains element MER11 repetitive element ;, mRNA sequence.

ACCESSION AI380618
VERSION AI380618.1 GI:4190471
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 472)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D. Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 407 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 444.

Location/Qualifiers
1. .472
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2107575"
/clone_lib="NCI_CGAP_CLL1"
/tissue_type="B-cell, chronic lymphocytic leukemia"
/lab_host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand CDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAATGGGCGCGCATGCTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento

Soares and M.Fatima Bonaldo."

BASE COUNT 161 a 103 c 42 g 166 t
ORIGIN

Query Match 2.2%; Score 26; DB 10; Length 472;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 27 ATTATTTCRAAAAAAAAAAAAAAAAAA 2

RESULT 27
BI297090/c

LOCUS BI297090 476 bp mRNA EST 19-JUL-2001
DEFINITION UI-R-DKO-cdt-b-09-0-UI.s1 UI-R-DKO Rattus norvegicus cDNA clone
UI-R-DKO-cdt-b-09-0-UI 3', mRNA sequence.

ACCESSION BI297090
VERSION BI297090.1 GI:14962158
KEYWORDS EST.
SOURCE Norway rat.

ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 476)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu

The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
normalized rat placenta pool library cDNA library preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com) the following repetitive
elements were found in this cDNA sequence: 1-51,
>AT_rich#Low_complexity 385-471, >PB1D10#SINE/Alu
Seq primer: M13 Forward
POLYA=Yes.

Location/Qualifiers
1. .476
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-DKO-cdt-b-09-0-UI"
/clone_lib="UI-R-DKO"
/dev_stage="ADULT"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-DKO
library is a subtracted library derived from a mixture of
five individually tagged normalized rat libraries:
brain-nRBP (20%), heart-nRBP (20%), kidney-nRBP (20%),
aorta-nRAP (20%), and placenta-nRBP (20%). Each original
library was constructed from a mixture of equal amounts of
RNA from seven different developmental time-points:
embryonic day 17, embryonic day 19, embryonic day 21,
adult day 1, adult day 12, adult day 75, and adult day
200. (Exception: the aorta pool does not contain embryonic
day 17 RNA and the placenta pool contains only the three

FEATURES
source

embryonic stages). Each library was normalized individually according to the procedure described by Ronaldo, Lennon & Soares (Genome Research 6: 791-806, 1996). For construction of the DKO subtracted library, plasmid DNA from each of the five individually tagged normalized libraries was mixed in the proportions specified above and electroporated into competent bacteria for production of single-stranded circular DNA representing the pool of libraries. Single-stranded circular DNA representing these five normalized libraries was then used as a tracer in a subtractive hybridization with a driver (PCR amplified inserts from a plasmid DNA template preparation) comprising: a) a set of about 1,000 arrayed clones from each of the five non-normalized libraries of brain (CTOs), heart (CSOs), kidney (CUOs), aorta (CWOs), and placenta (CXOs). The resulting pool of approximately 5,000 clones represented about 33.3% of the final driver population. A set of about 2,000 arrayed clones from each of the five normalized libraries of brain (CTO), heart (CSO), kidney (CUO), aorta (CWO), and placenta (CXO). The resulting pool of about 10,000 clones represented about 66.6% of the final driver population.

TAG-lib-UI-R-DKO
TAG-TISSUE-rat placenta pool
TAG_SEQ=TCACGACAGT

BASE COUNT 151 a 92 c 73 g 159 t 1 others
ORIGIN

Query Match 2.2%; Score 26; DB 11; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attattcaaaaaa1173

Db 26 ATTATTTCAAAAAA1173

RESULT 28

AI302809/c

LOCUS

DEFINITION

qns8904.xl NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1902486 3',

mRNA sequence.

AI302809

VERSION

AI302809.1 GI:39621155

KEYWORDS

EST

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheraia; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 488)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapb-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Greg Lennon, Ph.D.

Clone Distribution by: Washington University Genome Sequencing Center

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 373 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 450.

FEATURES

Location/Qualifiers

1. 488
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1902486"

embryonic stages). Each library was normalized individually according to the procedure described by Ronaldo, Lennon & Soares (Genome Research 6: 791-806, 1996). For construction of the DKO subtracted library, plasmid DNA from each of the five individually tagged normalized libraries was mixed in the proportions specified above and electroporated into competent bacteria for production of single-stranded circular DNA representing the pool of libraries. Single-stranded circular DNA representing these five normalized libraries was then used as a tracer in a subtractive hybridization with a driver (PCR amplified inserts from a plasmid DNA template preparation) comprising: a) a set of about 1,000 arrayed clones from each of the five non-normalized libraries of brain (CTOs), heart (CSOs), kidney (CUOs), aorta (CWOs), and placenta (CXOs). The resulting pool of approximately 5,000 clones represented about 33.3% of the final driver population. A set of about 2,000 arrayed clones from each of the five normalized libraries of brain (CTO), heart (CSO), kidney (CUO), aorta (CWO), and placenta (CXO). The resulting pool of about 10,000 clones represented about 66.6% of the final driver population.

TAG-lib-UI-R-DKO
TAG-TISSUE-rat placenta pool
TAG_SEQ=TCACGACAGT

BASE COUNT 151 a 92 c 73 g 159 t 1 others
ORIGIN

Query Match 2.2%; Score 26; DB 11; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attattcaaaaaa1173

Db 26 ATTATTTCAAAAAA1173

RESULT 28

AI302809/c

LOCUS

DEFINITION

qns8904.xl NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1902486 3',

mRNA sequence.

AI302809

VERSION

AI302809.1 GI:39621155

KEYWORDS

EST

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheraia; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 488)

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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapb-r@mail.nih.gov

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Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Greg Lennon, Ph.D.

Clone Distribution by: Washington University Genome Sequencing Center

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www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 373 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 450.

FEATURES

Location/Qualifiers

1. 488
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1902486"

embryonic stages). Each library was normalized individually according to the procedure described by Ronaldo, Lennon & Soares (Genome Research 6: 791-806, 1996). For construction of the DKO subtracted library, plasmid DNA from each of the five individually tagged normalized libraries was mixed in the proportions specified above and electroporated into competent bacteria for production of single-stranded circular DNA representing the pool of libraries. Single-stranded circular DNA representing these five normalized libraries was then used as a tracer in a subtractive hybridization with a driver (PCR amplified inserts from a plasmid DNA template preparation) comprising: a) a set of about 1,000 arrayed clones from each of the five non-normalized libraries of brain (CTOs), heart (CSOs), kidney (CUOs), aorta (CWOs), and placenta (CXOs). The resulting pool of approximately 5,000 clones represented about 33.3% of the final driver population. A set of about 2,000 arrayed clones from each of the five normalized libraries of brain (CTO), heart (CSO), kidney (CUO), aorta (CWO), and placenta (CXO). The resulting pool of about 10,000 clones represented about 66.6% of the final driver population.

TAG-lib-UI-R-DKO
TAG-TISSUE-rat placenta pool
TAG_SEQ=TCACGACAGT

BASE COUNT 151 a 92 c 73 g 159 t 1 others
ORIGIN

Query Match 2.2%; Score 26; DB 11; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attattcaaaaaa1173

Db 26 ATTATTTCAAAAAA1173

RESULT 28

AI302809/c

LOCUS

DEFINITION

qns8904.xl NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1902486 3',

mRNA sequence.

AI302809

VERSION

AI302809.1 GI:39621155

KEYWORDS

EST

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheraia; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 488)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapb-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Greg Lennon, Ph.D.

Clone Distribution by: Washington University Genome Sequencing Center

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 373 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 450.

FEATURES

Location/Qualifiers

1. 488
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1902486"

embryonic stages). Each library was normalized individually according to the procedure described by Ronaldo, Lennon & Soares (Genome Research 6: 791-806, 1996). For construction of the DKO subtracted library, plasmid DNA from each of the five individually tagged normalized libraries was mixed in the proportions specified above and electroporated into competent bacteria for production of single-stranded circular DNA representing the pool of libraries. Single-stranded circular DNA representing these five normalized libraries was then used as a tracer in a subtractive hybridization with a driver (PCR amplified inserts from a plasmid DNA template preparation) comprising: a) a set of about 1,000 arrayed clones from each of the five non-normalized libraries of brain (CTOs), heart (CSOs), kidney (CUOs), aorta (CWOs), and placenta (CXOs). The resulting pool of approximately 5,000 clones represented about 33.3% of the final driver population. A set of about 2,000 arrayed clones from each of the five normalized libraries of brain (CTO), heart (CSO), kidney (CUO), aorta (CWO), and placenta (CXO). The resulting pool of about 10,000 clones represented about 66.6% of the final driver population.

TAG-lib-UI-R-DKO
TAG-TISSUE-rat placenta pool
TAG_SEQ=TCACGACAGT

BASE COUNT 151 a 92 c 73 g 159 t 1 others
ORIGIN

Query Match 2.2%; Score 26; DB 11; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attattcaaaaaa1173

Db 26 ATTATTTCAAAAAA1173

RESULT 28

AI302809/c

LOCUS

DEFINITION

qns8904.xl NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1902486 3',

mRNA sequence.

AI302809

VERSION

AI302809.1 GI:39621155

KEYWORDS

EST

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheraia; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 488)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapb-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Greg Lennon, Ph.D.

Clone Distribution by: Washington University Genome Sequencing Center

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 373 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 450.

FEATURES

Location/Qualifiers

1. 488
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1902486"

embryonic stages). Each library was normalized individually according to the procedure described by Ronaldo, Lennon & Soares (Genome Research 6: 791-806, 1996). For construction of the DKO subtracted library, plasmid DNA from each of the five individually tagged normalized libraries was mixed in the proportions specified above and electroporated into competent bacteria for production of single-stranded circular DNA representing the pool of libraries. Single-stranded circular DNA representing these five normalized libraries was then used as a tracer in a subtractive hybridization with a driver (PCR amplified inserts from a plasmid DNA template preparation) comprising: a) a set of about 1,000 arrayed clones from each of the five non-normalized libraries of brain (CTOs), heart (CSOs), kidney (CUOs), aorta (CWOs), and placenta (CXOs). The resulting pool of approximately 5,000 clones represented about 33.3% of the final driver population. A set of about 2,000 arrayed clones from each of the five normalized libraries of brain (CTO), heart (CSO), kidney (CUO), aorta (CWO), and placenta (CXO). The resulting pool of about 10,000 clones represented about 66.6% of the final driver population.

TAG-lib-UI-R-DKO
TAG-TISSUE-rat placenta pool
TAG_SEQ=TCACGACAGT

BASE COUNT 151 a 92 c 73 g 159 t 1 others
ORIGIN

Query Match 2.2%; Score 26; DB 11; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attattcaaaaaa1173

Db 26 ATTATTTCAAAAAA1173

RESULT 28

AI302809/c

LOCUS

DEFINITION

qns8904.xl NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1902486 3',

mRNA sequence.

AI302809

VERSION

AI302809.1 GI:39621155

KEYWORDS

EST

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheraia; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 488)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapb-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Greg Lennon, Ph.D.

Clone Distribution by: Washington University Genome Sequencing Center

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 373 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 450.

FEATURES

Location/Qualifiers

1. 488
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1902486"

embryonic stages). Each library was normalized individually according to the procedure described by Ronaldo, Lennon & Soares (Genome Research 6: 791-806, 1996). For construction of the DKO subtracted library, plasmid DNA from each of the five individually tagged normalized libraries was mixed in the proportions specified above and electroporated into competent bacteria for production of single-stranded circular DNA representing the pool of libraries. Single-stranded circular DNA representing these five normalized libraries was then used as a tracer in a subtractive hybridization with a driver (PCR amplified inserts from a plasmid DNA template preparation) comprising: a) a set of about 1,000 array

/sex="mixed"
 /tissue_type="26 somite embryos, adult livers, shield stage embryos"
 /lab_host="X11-blue MRF"
 /note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; 1st strand cDNA was primed with a Not I - oligo(dT)15 primer [5'-pGACTAGTCTCATGCGGCGCGCGCTTTTCTTTTCTTTT3']; double-stranded cDNA was ligated to Sal I adaptors (BRL), digested with Not I and cloned into the Not I and Sal I sites of the pSPORT1 vector (BRL). Library was constructed by Matthew Clark (Lehrach lab; ICRF, London and Max Planck Institut fuer Molekulare Genetik, Berlin). cDNAs for EST analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality control."

BASE COUNT 175 a 68 c 69 g 178 t
 ORIGIN

Query Match 2.2%; Score 26; DB 10; Length 490;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaa 1173
 |||||||
 Db 39 ATTATTTCAAAAAA 14

RESULT 30
 AL382797
 LOCUS AL382797 510 bp mRNA EST 03-AUG-2000
 DEFINITION MTBC10A07R1 MtBC Medicago truncatula cDNA clone MtBC10A07 T7, mRNA sequence.
 ACCESSION AL382797
 VERSION AL382797.1 GI:9682548
 KEYWORDS EST.
 SOURCE barrel medic.
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
 REFERENCE 1 (bases 1 to 510)
 AUTHORS Journet,E.P., Crespeau,H., van-Tuinen,D., Gouzy,J., Jaillon,O., Niebel,A., Carreau,V., Chatagnier,O., Kahn,D., Gianinazzi-Pearson V. and Gamas,P.
 TITLE Medicago truncatula ESTs from endomycorrhizal roots
 JOURNAL Unpublished (2000)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de Biologie Moleculaire des Relations Plantes-Microorganismes, CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email : mt-est@toulouse.inra.fr Website : http://sequence.toulouse.inra.fr/Mtruncatula.html).
 FEATURES
 source Location/Qualifiers
 1..510
 /organism="Medicago truncatula"
 /cultivar="Jemalong"
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 /clone="MTBC10A07"
 /clone_lib="MTBC"
 /tissue_type="arbuscular mycorrhiza"
 /dev_stage="harvested 3 weeks post inoculation with Glomus

intraradices"
 /note="Vector: pBluescript pSK; Site_1: EcoRI; Site_2: XhoI; M. truncatula sterilised seeds were germinated for 72h at 25 C, before transplanting into a 1/3 Epioisses soil : 2/3 calcined terragreen mix in the presence of onion root fragments colonized by the arbuscular mycorrhizal fungus Glomus intraradices (Schenck & Smith, isolate LP48). The plants were watered every day and twice a week with a modified nutrient Long Ashton solution without phosphate but with a high level of nitrate. After 3 weeks RNA was extracted from whole root systems. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-Zap XR vector from Stratagene and packaged using Gigapack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using ExAssit helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Evry, France). Note : EST may be of fungal origin."

BASE COUNT 191 a 51 c 46 g 222 t
 ORIGIN

Query Match 2.2%; Score 26; DB 10; Length 510;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaa 1173
 |||||||
 Db 483 ATTATTTCAAAAAA 508

RESULT 31
 AI974955/c
 LOCUS AI974955 513 bp mRNA EST 27-AUG-1999
 DEFINITION EST269549 Schistosoma mansoni female, Phil Loverde/Joe Merrick Schistosoma mansoni cDNA clone SMFAA16 5' end similar to actin, mRNA sequence.
 ACCESSION AI974955
 VERSION AI974955.1 GI:5788123
 KEYWORDS EST.
 SOURCE Schistosoma mansoni.
 ORGANISM Schistosoma mansoni
 Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths; Rhabditophora; Eulecithophora; Revertospermatia; Mediofusata; Neodermata; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
 REFERENCE 1 (bases 1 to 513)
 AUTHORS Merrick,J.M., Osman,A., Loverde,P.T., Chandra,I., Glodek,A., Fraser ,C.M. and Lee,N.H.
 TITLE Generation of a Schistosoma sp. EST (SMEST) Catalog & Schistosome Gene Index
 JOURNAL Unpublished (1998)
 COMMENT Contact: Norman H. Lee
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 3529
 Fax: 301 838 0208
 Email: nhlee@tigr.org
 Seq primer: M13 Reverse.
 FEATURES
 source Location/Qualifiers
 1..513
 /organism="Schistosoma mansoni"
 /db_xref="taxon:6183"
 /clone="SMFAA16"
 /clone_lib="Schistosoma mansoni female, Phil Loverde/Joe Merrick"
 /sex="female"
 /note="Vector: pBluescript SK; Site_1: EcoRI; Site_2: XhoI ; directionally cloned cDNAs"
 BASE COUNT 151 a 110 c 88 g 164 t
 ORIGIN

Query Match 2.2%; Score 26; DB 10; Length 513;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1148 attatttcaaaaaa1173
 Db 66 ATTATTTCAAAAA1173

RESULT 32
 AW066395/c 530 bp mRNA EST 30-MAR-2000
 LOCUS 687001H02.y1 687 - Early embryo from Delaware Zea mays cDNA, mRNA
 DEFINITION
 ACCESSION AW066395
 VERSION AW066395.1 GI:6021467
 KEYWORDS EST.
 SOURCE Zea mays.
 ORGANISM Zea mays.

REFERENCE
 AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 TITLE Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 JOURNAL clade; Panicoidae; Andropogoneae; Zea.
 COMMENT 1 (bases 1 to 530)

Maize ESTs from various cDNA libraries sequenced at Stanford
 University
 Unpublished (1999)
 CONTACT: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 687001 row: H column: 02.

FEATURES
 source
 1..530
 /organism="Zea mays"
 /cultivar="Illinois High Oil"
 /db_xref="taxon:4577"
 /clone_lib="687 - Early embryo from Delaware"
 /tissue_type="embryo"
 /dev_stage="14, 21, 28, and 35 days after pollination"
 /lab_host="E. coli SOLR"
 /note="Organ: embryo; Vector: pBluescript SK; Site_1: xhoI
 ; Site_2: EcoRI; Library was prepared by Statagene using
 the Uni-ZAP XR system (Stratagene BN937328-12). Clones
 were picked by a Q-bot after blue/white selection
 (ampicillin resistance - use 100 micrograms/microliter).
 Developed from a pool of equal amounts of RNA from
 developing embryos sampled at 14, 21, 28 and 35 days after
 pollination of the Illinois High Oil Maize Strain Cycle
 90. This closed strain has been selected for high oil
 concentration for 90 generations and originates from the
 1890s era open pollinated variety Burr's White"

BASE COUNT 147 a 116 c 112 g 155 t
 ORIGIN
 Query Match 2.2%; Score 26; DB 10; Length 530;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1148 attatttcaaaaaa1173
 Db 54 ATTATTTCAAAAA1173

RESULT 33
 AW700042/c 546 bp mRNA EST 18-APR-2000
 LOCUS gb37h12.y1 Moss EST library PPN Physcomitrella patens cDNA clone
 DEFINITION

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS

TITLE
 JOURNAL
 COMMENT

FEATURES
 source

1..546
 /organism="Physcomitrella patens"
 /db_xref="taxon:3218"
 /clone_lib="Moss EST library PPN"
 /tissue_type="protonemata: 7 day old tissue auxin treated"
 /lab_host="DH10B"
 /note="Vector: pBluescript SK; Site_1: EcoRI; Site_2:
 xhoI; Construction of the cDNA library was carried out
 using Stratagene's 'Unizap - cDNA synthesis kit'. cDNA was
 constructed using an oligo dT primer/linker that contains
 a XhoI site within it. Following ds cDNA synthesis,
 EcoRI adapters were ligated to the blunt ends and sample
 was digested with XhoI. The result is cDNA with an EcoRI
 sticky end on one side and a XhoI sticky end on the other.
 This cDNA was ligated directionally in Unizap arms. The
 vector is designed containing the pBluescript sequence as
 well as lambda DNA and cDNA is cloned within this
 pBluescript sequence. The vector was then packaged using
 Gold gigaPackaging extracts. Library was grown in XlBlue
 MRF' cells and amplified. The library was excised by mass
 excision using Stratagene's 'Mass excision kit' that uses
 exsist as a helper phage that releases the pBluescript
 sequence and circularises it as single stranded plasmids
 that are then packaged (by helper phage) and secreted out
 of the host cell as phagemids. SOLR cells were transformed
 with phagemids and the library was plated out on LB-amp
 plates to select for transformants. Approximately 1,000
 ,000 colonies were grown and recovered. The double
 stranded plasmid library was recovered by using Qulagen
 Midi prep kit. 2 micro grams of each library were used to
 transform DH10B cells by electroporation."

BASE COUNT 153 a 143 c 100 g 150 t
 ORIGIN

Query Match 2.2%; Score 26; DB 10; Length 546;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1148 attatttcaaaaaa1173

|||||
Db 39 ATTATTTCAAAAAAAAAAAAAAAAAA 14

RESULT 34

AW067352/c

LOCUS

DEFINITION

mays cDNA, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PAC

1 (bases 1 to 554)

Walbot, V.

University

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 683022 row: G column: 01.

Location/Qualifiers

1. .554

/organism="Zea mays"

/cultivar="B73"

/db_xref="taxon:4577"

/clone_lib="683 - 14 day immature embryo from Hake lab (HS)"

/tissue_type="embryo"

/dev_stage="14 days after pollination"

/lab_host="DH10B"

/note="Organ: embryo; Vector: pBKMV (Stratagene's zap Express); Site_1: XhoI; Site_2: EcoRI; Directionally cloned, 14 day immature embryo library created with Stratagene's Zap Express cDNA protocol."

BASE COUNT

153 a 151 c 122 g 128 t

ORIGIN

Query Match

Best Local Similarity

Matches

26; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY 1148 attatttcaaaaaaaaaaaaaaaaaa 1173

|||||

Db 29 ATTATTTCAAAAAAAAAAAAAAAAAA 4

RESULT 35

AI450987/c

LOCUS

DEFINITION

mt12f02.x1 Soares mouse 3NDMS Mus musculus cDNA clone IMAGE:620859

3' similar to TR:Q13535 Q13535 FRAP-RELATED PROTEIN ;, mRNA

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 584)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person

B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu

TITLE
JOURNAL
COMMENT

Unpublished (1999)

Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

This clone was previously sequenced on the 5' end only, this new

data is from the 3' end

Possible reversed clone: similarity on wrong strand

High quality sequence stop: 228.

Location/Qualifiers

1. .584

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone_image="IMAGE:620859"

/clone_lib="Soares mouse 3NDMS"

/sex="male"

/tissue_type="Spleen"

/dev_stage="4 weeks"

/lab_host="DH10B"

/note="Vector: p7T3D-Pac (Pharmacia) with a modified

polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA

was primed with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAAGTGGAGCGCGCGCTTTTTTTTTTTTTTTTTTTTTTTTTTTT

3']; double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified p7T3 vector. RNA

provided by Dr. Bertrand Jordan. Library went through

three rounds of normalization, and was constructed by

Bento Soares and M.Fatima Bonaldo."

BASE COUNT

155 a 132 c 103 g 194 t

ORIGIN

Query Match

Best Local Similarity

Matches

26; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY 1148 attatttcaaaaaaaaaaaaaaaaaa 1173

|||||

Db 27 ATTATTTCAAAAAAAAAAAAAAAAAA 2

RESULT 36

BF646151

LOCUS

DEFINITION

clone NF067A10EC2 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;

Medicago.

1 (bases 1 to 618)

Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation -

Center for Medicago Genomics Research

Unpublished (2000)

Contact: Dixon RA

Plant Biology Division

Plant Biology Division

Plant Biology Division

Plant Biology Division

Plant Biology Division

Plant Biology Division

Plant Biology Division

Plant Biology Division

Plant Biology Division

The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380

Email: radixon@noble.org
Insert Length: 618 Std Error: 0.00
Plate: 067 row: A column: 10
Seq primer: TCACACGAGAAACAGCTATGAC.

FEATURES

Location/Qualifiers
1. .618
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF067A10EC"
/clone_lib="Elicited cell culture"
/tissue_type="Cell cultures derived from root tissues"
/dev_stage="Cell suspensions were subcultured every 14 days. Cells were induced six days after subculture"
/note="Vector: Lambda zap; Cells were induced with yeast cell wall extracts equivalent to 50ug/ml glucose in the final concentration. Samples were taken at 0.5, 1, 12 and 24 hours after induction. Equal amounts of RNA from each time point were pooled and used for mRNA isolation."
211 a 119 c 119 g 167 t 2 others

BASE COUNT

211 a 119 c 119 g 167 t 2 others

ORIGIN

Query Match 2.2%; Score 26; DB 11; Length 618;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaa 1173

||||| 1173

Db 585 ATTATTTCAAAAAA 610

RESULT 37

AZ369897/c
LOCUS 623 bp DNA GSS 02-OCT-2000
DEFINITION LM0120N12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0120N12 R, DNA sequence.

ACCESSION AZ369897

VERSION AZ369897.1 GI:10483597

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 623)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0120 row: N column: 12

Seq primer: CACACGAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 623.

Location/Qualifiers

1. .623

FEATURES

source

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0120N12"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 182 a 104 c 119 g 217 t 1 others
ORIGIN

Query Match 2.2%; Score 26; DB 13; Length 623;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaa 1173

||||| 1173

Db 219 ATTATTTCAAAAAA 194

RESULT 38

BF294174/c

LOCUS 641 bp mRNA EST 04-MAY-2001

DEFINITION 001PB02 Pb cDNA #17, Tommaso Pace, Marta Ponzi, and Clara Frontali
Plasmodium berghei cDNA 5', mRNA sequence.

ACCESSION BF294174

VERSION BF294174.1

KEYWORDS GI:13942740

SOURCE EST.

ORGANISM Plasmodium berghei.

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases 1 to 641)

AUTHORS Carlton,J.M.-R. and Dame,J.B.

TITLE The Plasmodium vivax and P. berghei gene sequence tag projects

JOURNAL Parasitol. Today 16 (10), 409 (2000)

COMMENT Contact: Dame JB

Department of Pathobiology, College of Veterinary Medicine

University of Florida

2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611-0880, USA

Tel: 352 392 4700

Fax: 352 392 9704

Email: damej@mail.vetmed.ufl.edu

Seq primer: T3.

Location/Qualifiers

1. .641

source

/organism="Plasmodium berghei"

/strain="ANKA clone HP (gametocyte producer)"

/db_xref="taxon:5821"

/clone_lib="Pb cDNA #17, Tommaso Pace, Marta Ponzi, and Clara Frontali"

/dev_stage="asynchronous blood stage"

/lab_host="Wistar rats"

/note="Vector: pBluescript II vector DNA, excised from

Lambda ZAP II.; Site_1: ECORI; Site_2: XhoI; Total RNA was

extracted from asynchronous blood stage forms of the

cloned ANKA isolate of P. berghei, grown in Wistar rats to

30% parasitemia and 2-5% gametocytemia. Contaminating host

white cells had previously been removed and final host cell contamination estimated to be approximately 5%. PolyA+ RNA was extracted and reverse transcribed using an oligo dt-xhoI primer (Lambda ZAP II cDNA cloning kit, Stratagene). Second strand cDNA was made following the manufacturer's protocol. EcoRI adaptors were ligated to the cDNA, and fragments were ligated into EcoRI/XhoI digested vector."

```

BASE COUNT      278 a  67 c  63 g  233 t
ORIGIN

Query Match      2.2%; Score 26; DB 11; Length 641;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1148 attatttcaaaaaaaaaaaaaaaaaa 1173
Db 31 ATTATTTCAAAAAAAAAAAAAAAAAA 5

RESULT 39
BI094602      683 bp  mRNA      EST      20-JUN-2001
LOCUS      LBSSH00034 Preinfection stage symbiosis-regulated cDNAs from L.
DEFINITION bicolor x P. resinosa Laccaria bicolor cDNA, mRNA sequence.
ACCESSION BI094602
VERSION BI094602.1 GI:14516079
KEYWORDS EST.
SOURCE Laccaria bicolor.
ORGANISM Laccaria bicolor
REFERENCE Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
AUTHORS Agaricales; Tricholomataceae; Laccaria.
TITLE 1 (bases 1 to 683)
JOURNAL Podila G.K., Brand J.R. and Hynes M.J.
COMMENT Preinfection stage symbiosis-regulated cDNAs from L. bicolor x P.
resinosa
Unpublished (2001)
Contact: Dr. G.K. Podila
Department of Biological Sciences
Michigan Technological University
1400 Townsend Drive, Houghton, MI 49931, USA
Tel: 906 487 3068
Fax: 906 487 3167
Email: gkpodila@mtu.edu.

FEATURES
source
1..683
/db_xref="taxon:29883"
/clone_lib="Preinfection stage symbiosis-regulated cDNAs
from L. bicolor x P. resinosa"
/notes="cDNA clones were selected using a combination of
Suppressive subtraction hybridization derived probes and
a cDNA library of L. bicolor, prepared from pooled RNA of
interaction time points ranging from 6-72 h. Differential
expression of these cDNAs was confirmed through screening
a membrane array of the cDNAs with exponential probes
prepared from control RNA obtained from free living L.
bicolor and pooled interaction RNA."

BASE COUNT      261 a  90 c  118 g  214 t
ORIGIN

Query Match      2.2%; Score 26; DB 11; Length 683;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1148 attatttcaaaaaaaaaaaaaaaaaa 1173
Db 647 ATTATTTCAAAAAAAAAAAAAAAAAA 672

RESULT 40

```

```

AW331967/c
LOCUS      718 bp  mRNA      EST      31-JAN-2000
DEFINITION SL16 AGS-1 Pneumocystis carinii f. sp. carinii cDNA 3', mRNA
sequence.
ACCESSION AW331967
VERSION AW331967.1 GI:6828233
KEYWORDS EST.
SOURCE Pneumocystis carinii f. sp. carinii.
ORGANISM Pneumocystis carinii f. sp. carinii
REFERENCE Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
AUTHORS Smulian, A.G., Arnold, J., Weise, M., Wunderlich, J., Staben, C., Edman,
J.C., Kovacs, J. and Cushion, M.
TITLE Expressed sequence tags from Pneumocystis carinii
JOURNAL Unpublished (2000)
COMMENT Contact: Staben C
School of Biological Sciences
University of Kentucky
101 Morgan Building, University of Kentucky, Lexington, KY
40506-0225, USA
Tel: 606 257 2161
Fax: 606 257 1717
Email: staben@pop.uky.edu.

FEATURES
source
1..718
/organism="Pneumocystis carinii f. sp. carinii"
/db_xref="taxon:38081"
/clone_lib="AGS-1"
/lab_host="E. coli"
/notes="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;
P. carinii organisms (3x10e9) from a single rat (99-1-6,
sacrificed on 3/17/99) at Cincinnati VA facilities.
Trizol extracted RNA. Oligo dT priming, standard
conditions described by vendor, Stratagene. Further
details see www.uky.edu/project/Pneumocystis/"

BASE COUNT      290 a  98 c  85 g  245 t
ORIGIN

Query Match      2.2%; Score 26; DB 10; Length 718;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1148 attatttcaaaaaaaaaaaaaaaaaa 1173
Db 26 ATTATTTCAAAAAAAAAAAAAAAAAA 1

RESULT 41
AW331951/c
LOCUS      794 bp  mRNA      EST      31-JAN-2000
DEFINITION SL11 AGS-1 Pneumocystis carinii f. sp. carinii cDNA 3', mRNA
sequence.
ACCESSION AW331951
VERSION AW331951.1 GI:6828217
KEYWORDS EST.
SOURCE Pneumocystis carinii f. sp. carinii.
ORGANISM Pneumocystis carinii f. sp. carinii
REFERENCE Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
AUTHORS Smulian, A.G., Arnold, J., Weise, M., Wunderlich, J., Staben, C., Edman,
J.C., Kovacs, J. and Cushion, M.
TITLE Expressed sequence tags from Pneumocystis carinii
JOURNAL Unpublished (2000)
COMMENT Contact: Staben C
School of Biological Sciences
University of Kentucky
101 Morgan Building, University of Kentucky, Lexington, KY
40506-0225, USA
Tel: 606 257 2161
Fax: 606 257 1717

```

```

Email: staben@pop.uky.edu.
Location/Qualifiers
1. .794
/organism="Pneumocystis carinii f. sp. carinii"
/db_xref="taxon:38081"
/clone_lib="AGS-1"
/lab_host="E. coli"
/note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
P. carinii organisms (3x10e9) from a single rat (99-1-6,
sacrificed on 3/17/99) at Cincinnati VA facilities.
Trizol extracted RNA. Oligo dt priming, standard
conditions described by vendor, Stratagene. Further
details see www.uky.edu/project/pneumocystis/"
BASE COUNT      278 a 135 c 113 g 268 t
ORIGIN

Query Match      2.2%; Score 26; DB 10; Length 794;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1148 attattcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 27 ATTATTTCAAAAAAAAAAAAAAAAAA 2

RESULT 42
BG151615/c      100 bp mRNA EST 05-FEB-2001
LOCUS
DEFINITION
naq62b09.x1 NCI_CGAP_Co26 Homo sapiens cDNA clone IMAGE:4225889 3',
mRNA sequence.
ACCESSION
BG151615
VERSION
BG151615.1 GI:12663645
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 100)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
cDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -400P from Gibco.
Location/Qualifiers
1. .100
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4225889"
/clone_lib="NCI_CGAP_Co26"
/tissue_type="normal colonic mucosa"
/lab_host="DH10B"
/note="Organ: colon; Vector: pAMP1; mRNA made from normal
colonic mucosa, cDNA made by oligo-dT priming.
Directionally cloned into UDG sites. Size-selected on
agarose gel, average insert size 300 bp. Primary library.
cDNA library preparation: David B. Krizman, Ph.D.
Reference: Krizman et al. (1996) Cancer Research
56:5380-5383."
BASE COUNT      25 a 22 c 13 g 40 t
ORIGIN

Query Match      2.1%; Score 25; DB 11; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 54 TTATTTCAAAAAAAAAAAAAAAAAA 30

RESULT 43
AI348819      151 bp mRNA EST 16-FEB-1999
LOCUS
DEFINITION
ta90e02.x2 NCI_CGAP_Brn20 Homo sapiens cDNA clone IMAGE:2051354 3',
mRNA sequence.
ACCESSION
AI348819
VERSION
AI348819.1 GI:4086025
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 151)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGP), Tumor Gene Index
JOURNAL
Unpublished (1998)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Robert Jenkins, M.D., Mark Israel, M.D., Jim
Jacobson, Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 235 Std Error: 0.00
Seq primer: -400P from Gibco.
Location/Qualifiers
1. .151
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2051354"
/clone_lib="NCI_CGAP_Brn20"
/tissue_type="oligodendroglioma"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: brain; Vector: pAMP1; mRNA made from
oligodendroglioma tissue, cDNA made by oligo-dT priming.
Directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."
BASE COUNT      71 a 16 c 27 g 37 t
ORIGIN

Query Match      2.1%; Score 25; DB 10; Length 151;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 107 TTATTTCAAAAAAAAAAAAAAAAAA 131

RESULT 44
BE162370      162 bp mRNA EST 21-JUN-2000
LOCUS
DEFINITION
PM2-HT0451-090100-002-b03 HT0451 Homo sapiens cDNA, mRNA sequence.
ACCESSION
BE162370
VERSION
BE162370.1 GI:8625091
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens

```



```

FEATURES
source
POLYA=Yes.
Location/Qualifiers
1. .181
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-CEI-bal-f-04-0-UI"
/clone_lib="NIH-BMAP_Ret3_N"
/dev_stage="6 weeks"
/lab_host="PH10B (Life Technologies)"
/note="Vector: pT73D-pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; The
NIH-BMAP_Ret3_N library is a normalized library derived
NIH-BMAP_Ret3. NIH-BMAP_Ret3 was made from mouse retina
tissue. For a detailed description of the library from
which this clone was derived, please visit our web site
at brainest.eng.uiowa.edu.
TAG_LIB=NIH-BMAP_Ret3_N
TAG_TISSUE=adult-retina
TAG_SEQ=GTCCGCGCAC"
BASE COUNT 39 a 42 c 38 g 62 t
ORIGIN

Query Match 2.1%; Score 25; DB 11; Length 181;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1148 attatttcaaaaaaaaaaaaaa 1172
Db 25 ATTATTTCAAAAAAAAAAAAAAAAA 1

RESULT 47
AL377517 202 bp mRNA EST 03-AUG-2000
LOCUS MLEB32B08R1 MtBB Medicago truncatula cDNA clone MtBB32B08 T7, mRNA
DEFINITION sequence.
ACCESSION AL377517
VERSION AL377517.1 GI:9677269
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 202)
Journet,E.P., Crespeau,H., van-Tuinen,D., Gouzy,J., Jaillon,O.,
Niebel,A., Carreau,V., Chatagnier,O., Kahn,D., Gianinazzi-Pearson
,V. and Gamas,P.
Medicago truncatula ESTs from Sinorhizobium meliloti-induced root
nodules
Unpublished (2000)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 2731326 Castanet-Tolosan Cedex, France (Email :
Mt-est@toulouse.inra.fr Website :
http://sequence.toulouse.inra.fr/Mtruncatula.html).
Location/Qualifiers
1. .202
/organism="Medicago truncatula"
/cultivar="Jemalong"
/db_xref="taxon:3880"
/clone="MTBB32B08"
/clone_lib="MtBB"
/tissue_type="symbiotic root nodules"
/dev_stage="harvested 4 days post inoculation with
Sinorhizobium meliloti"

FEATURES
source
POLYA=Yes.
Location/Qualifiers
1. .218
/organism="Aspergillus niger"
/db_xref="taxon:5061"
/clone="1998"
/clone_lib="Aspergillus niger, pYES2 (XhoI-EcoRI)"
/lab_host="E. coli"
/note="Vector: pYES2; site 1: Xho-I; Site 2: EcoRI; cDNA
was synthesized with ZAP kit (Stratagene) using poly(A)+
RNA isolated from Aspergillus niger grown in both complete
and minimal media. Synthesis was primed with oligo(dT)
primer/XhoI-linker. EcoRI adaptors were later ligated to
polished ends. EcoRI-XhoI-digested cDNA was ligated with
EcoRI-XhoI-digested pYES2 (Invitrogen Corp). This vector
permits expression of our library in yeast."
BASE COUNT 61 a 52 c 30 g 71 t 4 others
ORIGIN

/note="Vector: pBluescript PSK; Site 1: EcoRI; Site 2:
XhoI; Plants were grown in an aeroponic chamber on
nitrogen-rich medium for 21 days. Three days before
inoculation with Sinorhizobium meliloti, the medium was
replaced by N-free medium. Root nodules (+ short adjacent
root segments) were harvested 4 days post inoculation.
cDNA was prepared from polyA+ enriched RNA. The cDNA was
directionally ligated into Uni-zap XR vector from
Stratagene and packaged using Gigapack Gold packaging
extracts. Plasmids containing cDNA inserts were
mass-excised from phage stocks using Exsist helper phage
and propagated in SOLR cells. Clone ordering and
sequencing was performed by the Centre National de
Sequencage (Genoscope, Evry, France)."
BASE COUNT 57 a 34 c 25 g 86 t
ORIGIN

Query Match 2.1%; Score 25; DB 10; Length 202;
Best Local Similarity 100.0%; Pred. No. 6.3e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1149 ttatttcaaaaaaaaaaaaaa 1173
Db 175 TTATTTCAAAAAAAAAAAAAAAAA 199

RESULT 48
BE760641 218 bp mRNA EST 24-OCT-2000
LOCUS an.1998 Aspergillus niger, pYES2 (XhoI-EcoRI) Aspergillus niger
DEFINITION cDNA clone 1998 3', mRNA sequence.
ACCESSION BE760641
VERSION BE760641.1 GI:10183278
KEYWORDS EST.
SOURCE Aspergillus niger.
ORGANISM Aspergillus niger.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
1 (bases 1 to 218)
Tsang,A. and Storms,R.
Aspergillus niger Expressed Sequence Tags
Unpublished (2000)
Contact: Tsang, A.
Dept. of Biology
Concordia University
1455 deMaisonneuve Blvd. West, Montreal, Quebec, CANADA, H3G 1M8
Tel: 514-848-3405
Fax: 514-848-4504
Email: tsang@vax2.concordia.ca
PCR PRIMERS
BACKWARD: GCGGTGAATGTACGCGTGACATAAC
Insert Length: 218 Std Error: 0.00
POLYA=Yes.
Location/Qualifiers
1. .218
/organism="Aspergillus niger"
/db_xref="taxon:5061"
/clone="1998"
/clone_lib="Aspergillus niger, pYES2 (XhoI-EcoRI)"
/lab_host="E. coli"
/note="Vector: pYES2; site 1: Xho-I; Site 2: EcoRI; cDNA
was synthesized with ZAP kit (Stratagene) using poly(A)+
RNA isolated from Aspergillus niger grown in both complete
and minimal media. Synthesis was primed with oligo(dT)
primer/XhoI-linker. EcoRI adaptors were later ligated to
polished ends. EcoRI-XhoI-digested cDNA was ligated with
EcoRI-XhoI-digested pYES2 (Invitrogen Corp). This vector
permits expression of our library in yeast."
BASE COUNT 61 a 52 c 30 g 71 t 4 others
ORIGIN

```

```

Query Match          2.1%; Score 25; DB 10; Length 218;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
Db 30 TTATTTCAAAAAAAAAAAAAAAAAA 6

RESULT 49
LOCUS AL383797 248 bp mRNA EST 03-AUG-2000
DEFINITION MtBC16H05R1 MtBC Medicago truncatula cDNA clone MtBC16H05 T7, mRNA
sequence.
ACCESSION AL383797
VERSION AL383797.1 GI:9683548
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 248)
AUTHORS Journeel,E.P., Crespeau,H., van-Tuinen,D., Gouzy,J., Jaillon,O.,
Niebel,A., Carreau,V., Chataigner,O., Kahn,D., Gianinazzi-Pearson
,V. and Gamas,P.
Medicago truncatula ESTs from endomycorrhizal roots
Unpublished (2000)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Contact : Pascal Gamas and Etienne-Pascal Journeel, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email :
Mt-est@toulouse.inra.fr Website :
http://sequence.toulouse.inra.fr/Mtruncatula.html).
FEATURES
source
Location/Qualifiers
1..248
/organism="Medicago truncatula"
/cultivar="Jemalong"
/db_xref="taxon:3880"
/clone="MtBC16H05"
/clone_lib="MtBC"
/tissue_type="arbuscular mycorrhiza"
/dev_stage="harvested 3 weeks post inoculation with Glomus
intraradices"
/note="vector: pBluescript pSK; Site_1: EcoRI; Site_2:
XhoI; M. truncatula sterilised seeds were germinated for
72h at 25 C, before transplanting into a 1/3 Epoisses soil
: 2/3 calcined Terragreen mix in the presence of onion
root fragments colonized by the arbuscular mycorrhizal
fungus Glomus intraradices (Schenck & Smith, isolate LPA8
). The plants were watered every day and twice a week with
a modified nutrient Long Ashton solution without phosphate
but with a high level of nitrate. After 3 weeks RNA was
extracted from whole root systems. cDNA was prepared from
polyA+ enriched RNA. The cDNA was directionally ligated
into Uni-zap XR vector from Stratagene and packaged using
Gigapack Gold packaging extracts. Plasmids containing cDNA
inserts were mass-excised from phage stocks using Exasit
helper phage and propagated in SOLR cells. Clone ordering
and sequencing was performed by the Centre National de
Sequencage (Genoscope, Evry, France). Note : EST may be of
fungal origin."
BASE COUNT 70 a 45 c 42 g 91 t
ORIGIN

Query Match          2.1%; Score 25; DB 10; Length 248;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
Db 140 TTATTTCAAAAAAAAAAAAAAAAAA 164

BASE COUNT 156 a 11 c 10 g 72 t
ORIGIN

Query Match          2.1%; Score 25; DB 11; Length 249;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
Db 140 TTATTTCAAAAAAAAAAAAAAAAAA 164

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Search completed: December 27, 2001, 15:17:50
Job time: 1722 sec

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QY 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
Db 222 TTATTTCAAAAAAAAAAAAAAAAAA 246

RESULT 50
LOCUS BG894227 249 bp mRNA EST 04-JUN-2001
DEFINITION Kt09B02.y1 strongyloides ratti L1 pAMP1 v3 Chiapelli McCarter
Strongyloides ratti cDNA 5', mRNA sequence.
ACCESSION BG894227
VERSION BG894227.1 GI:14288837
KEYWORDS EST.
SOURCE Strongyloides ratti.
ORGANISM Strongyloides ratti
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Strongyloidea; Strongyloides.
REFERENCE 1 (bases 1 to 249)
AUTHORS McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T.,
Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.,
Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagaris,I., R.,
Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe
,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,
Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
Wilson,R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Brandi Chiapelli and Dr. James
McCarter (chiapell@watson.wustl.edu & jmccarter@watson.wustl.edu) at
Washington University, St. Louis. DNA Sequencing by: Washington
University Genome Sequencing Center St. Louis.
High quality sequence stop: 244.
FEATURES
source
Location/Qualifiers
1..249
/organism="Strongyloides ratti"
/db_xref="taxon:34506"
/clone_lib="Strongyloides ratti L1 pAMP1 v3 Chiapelli
McCarter"
/dev_stage="L1"
/lab_host="DH10B"
/note="Vector: pAMP1 (Gibco); The library was constructed
by Brandi Chiapelli and Dr. James McCarter at Washington
University, St. Louis. The cDNA was made by using
Dynabead oligo-dT priming (Dyna), PCR based library
using a modified protocol from the SMART PCR cDNA
Synthesis Kit from Clontech. Directionally cloned into the
UDG sites of pAMP1. Nematodes were provided by Dr. Mark
Viney of Bristol, UK."
BASE COUNT 156 a 11 c 10 g 72 t
ORIGIN

Query Match          2.1%; Score 25; DB 11; Length 249;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
Db 140 TTATTTCAAAAAAAAAAAAAAAAAA 164

```


101	1.9	35100	5	PCT-US93-06251-19	Sequence 19, Appl	174	21	1.8	1660	1	US-08-626-994A-2	Sequence 2, Appl
102	1.9	56516	2	US-08-996-306-1	Sequence 1, Appl	175	21	1.8	1660	3	US-08-957-742-2	Sequence 2, Appl
103	1.9	56516	4	US-09-338-907-1	Sequence 1, Appl	176	21	1.8	1669	4	US-09-461-697-184	Sequence 184, App
104	2.2	56520	4	US-09-338-907-179	Sequence 179, App	177	21	1.8	1710	3	US-09-000-630C-1	Sequence 1, Appl
105	2.1	30	4	US-08-817-787-30	Sequence 30, Appl	178	21	1.8	1710	3	US-08-862-730C-1	Sequence 2, Appl
106	2.1	1.8	76	US-08-931-859E-139	Sequence 139, App	179	21	1.8	1720	3	US-08-705-771-2	Sequence 1, Appl
107	2.1	1.8	76	US-08-981-732-139	Sequence 139, App	180	21	1.8	1752	4	US-09-360-779-1	Sequence 1, Appl
108	2.1	1.8	383	US-09-020-956-82	Sequence 82, App	181	21	1.8	1849	2	US-08-912-227-1	Sequence 1, Appl
109	2.1	1.8	383	US-09-030-607-82	Sequence 82, App	182	21	1.8	1858	4	US-09-347-819-1	Sequence 1, Appl
110	2.1	1.8	384	US-09-030-607-183	Sequence 183, App	183	21	1.8	1869	3	US-08-966-318-4	Sequence 4, Appl
111	2.1	1.8	391	US-08-253-155A-24	Sequence 24, Appl	184	21	1.8	1969	4	US-09-216-619-4	Sequence 4, Appl
112	2.1	1.8	392	US-08-253-155A-60	Sequence 60, Appl	185	21	1.8	2070	1	US-08-486-342-1	Sequence 1, Appl
113	2.1	1.8	488	US-09-385-982-471	Sequence 471, App	186	21	1.8	2070	1	US-08-473-092-1	Sequence 1, Appl
114	2.1	1.8	575	US-08-554-659-11	Sequence 11, App	187	21	1.8	2070	1	US-08-614-801A-1	Sequence 1, Appl
115	2.1	1.8	599	US-09-328-111-147	Sequence 11, App	188	21	1.8	2076	1	US-08-066-371-1	Sequence 1, Appl
116	2.1	1.8	604	US-09-328-111-391	Sequence 11, App	189	21	1.8	2076	4	US-09-042-494-1	Sequence 1, Appl
117	2.1	1.8	684	US-08-226-264-27	Sequence 27, App	190	21	1.8	2076	5	PCT-US94-05666-1	Sequence 1, Appl
118	2.1	1.8	723	US-08-618-911-1	Sequence 1, Appl	191	21	1.8	2114	1	US-07-803-622B-6	Sequence 1, Appl
119	2.1	1.8	737	US-08-602-262-1	Sequence 1, Appl	192	21	1.8	2207	4	US-08-956-322-3	Sequence 3, Appl
120	2.1	1.8	737	US-08-602-262-3	Sequence 3, Appl	193	21	1.8	2329	4	US-08-956-322-1	Sequence 1, Appl
121	2.1	1.8	737	US-09-004-716-1	Sequence 1, Appl	194	21	1.8	2336	2	US-08-389-564B-2	Sequence 2, Appl
122	2.1	1.8	742	US-09-004-716-3	Sequence 3, Appl	195	21	1.8	2336	2	US-08-466-047B-2	Sequence 2, Appl
123	2.1	1.8	780	US-07-847-010-12	Sequence 12, App	196	21	1.8	2567	3	US-08-993-260-4	Sequence 4, Appl
124	2.1	1.8	780	US-08-540-804-36	Sequence 36, App	197	21	1.8	2634	3	US-08-949-386-37	Sequence 37, App
125	2.1	1.8	820	US-08-590-399-36	Sequence 36, App	198	21	1.8	2634	3	US-08-450-562-26	Sequence 26, App
126	2.1	1.8	858	US-09-475-316A-28	Sequence 28, App	199	21	1.8	2671	2	US-08-408-519-1	Sequence 1, Appl
127	2.1	1.8	893	US-09-475-316A-14	Sequence 14, App	200	21	1.8	2671	5	PCT-US95-03559-1	Sequence 1, Appl
128	2.1	1.8	893	US-08-276-452A-66	Sequence 66, App	201	21	1.8	2712	3	US-08-949-386-38	Sequence 38, App
129	2.1	1.8	900	US-08-798-744-66	Sequence 66, App	202	21	1.8	2712	3	US-08-450-562-38	Sequence 38, App
130	2.1	1.8	901	US-08-924-759-5	Sequence 5, Appl	203	21	1.8	2815	1	US-08-230-491A-1	Sequence 1, Appl
131	2.1	1.8	911	US-09-248-335-5	Sequence 5, Appl	204	21	1.8	2815	1	US-08-619-280A-1	Sequence 1, Appl
132	2.1	1.8	911	US-09-248-335-33	Sequence 33, App	205	21	1.8	2815	2	US-08-940-391-1	Sequence 1, Appl
133	2.1	1.8	967	US-08-248-335-51	Sequence 51, App	206	21	1.8	2818	3	US-08-982-493-7	Sequence 7, Appl
134	2.1	1.8	974	US-08-540-459-13	Sequence 13, App	207	21	1.8	2818	3	US-08-628-655-1	Sequence 1, Appl
135	2.1	1.8	1046	US-08-361-467B-4	Sequence 4, Appl	208	21	1.8	2970	3	US-08-949-386-37	Sequence 37, App
136	2.1	1.8	1046	US-08-484-332C-4	Sequence 4, Appl	209	21	1.8	2970	3	US-08-450-562-37	Sequence 37, App
137	2.1	1.8	1063	US-08-325-562-1	Sequence 1, Appl	210	21	1.8	3101	5	PCT-US93-06251-7	Sequence 7, Appl
138	2.1	1.8	1063	US-08-437-795-1	Sequence 1, Appl	211	21	1.8	3101	5	PCT-US93-06251-7	Sequence 7, Appl
139	2.1	1.8	1074	US-08-975-316-54	Sequence 54, App	212	21	1.8	3471	2	US-08-868-786-1	Sequence 2, Appl
140	2.1	1.8	1075	US-08-975-316-55	Sequence 55, App	213	21	1.8	3865	1	US-08-832-883-48	Sequence 48, App
141	2.1	1.8	1163	US-09-160-588-1	Sequence 1, Appl	214	21	1.8	3865	2	US-08-832-883-48	Sequence 48, App
142	2.1	1.8	1233	US-08-853-839-1	Sequence 1, Appl	215	21	1.8	7587	4	US-08-378-313-22	Sequence 22, App
143	2.1	1.8	1319	US-08-504-459-7	Sequence 7, Appl	216	21	1.8	8743	3	US-09-081-320-1	Sequence 1, Appl
144	2.1	1.8	1338	US-08-484-993B-7	Sequence 7, Appl	217	21	1.8	11492	4	US-08-991-840A-1	Sequence 1, Appl
145	2.1	1.8	1338	US-08-484-993B-7	Sequence 7, Appl	218	21	1.8	4403765	4	US-09-103-840A-1	Sequence 2, Appl
146	2.1	1.8	1338	US-08-484-993B-7	Sequence 7, Appl	219	21	1.8	4411529	4	US-09-103-840A-1	Sequence 2, Appl
147	2.1	1.8	1338	US-08-484-996A-7	Sequence 7, Appl	220	20	1.7	38	2	US-08-930-274-15	Sequence 15, Appl
148	2.1	1.8	1338	US-08-458-731-7	Sequence 7, Appl	221	20	1.7	38	4	US-09-454-704A-7	Sequence 7, Appl
149	2.1	1.8	1338	US-08-149-223A-7	Sequence 7, Appl	222	20	1.7	40	1	US-08-510-032A-4	Sequence 4, Appl
150	2.1	1.8	1338	US-08-114-072-1	Sequence 7, Appl	223	20	1.7	40	3	US-08-688-514-4	Sequence 4, Appl
151	2.1	1.8	1365	PCT-US94-09361-1	Sequence 1, Appl	224	20	1.7	40	4	US-09-306-290-15	Sequence 15, Appl
152	2.1	1.8	1428	US-09-118-442-5	Sequence 5, Appl	225	20	1.7	40	4	US-09-306-290-26	Sequence 26, App
153	2.1	1.8	1433	US-07-968-971A-11	Sequence 11, App	226	20	1.7	40	4	US-09-306-290-30	Sequence 30, App
154	2.1	1.8	1433	US-07-968-971A-11	Sequence 11, App	227	20	1.7	43	4	US-09-306-290-37	Sequence 37, App
155	2.1	1.8	1433	US-08-424-406-2	Sequence 2, App	228	20	1.7	46	2	US-08-930-274-16	Sequence 16, App
156	2.1	1.8	1433	US-08-464-523B-8	Sequence 8, App	229	20	1.7	115	2	US-08-930-274-11	Sequence 11, App
157	2.1	1.8	1433	US-08-464-523B-8	Sequence 8, App	230	20	1.7	123	2	US-08-153-051B-30	Sequence 30, App
158	2.1	1.8	1442	US-08-468-763-18	Sequence 18, App	231	20	1.7	142	1	US-08-060-952C-46	Sequence 46, App
159	2.1	1.8	1442	US-08-468-763-18	Sequence 18, App	232	20	1.7	142	1	US-08-151-477A-30	Sequence 30, App
160	2.1	1.8	1502	US-08-393-996A-18	Sequence 18, App	233	20	1.7	142	3	US-08-819-867-60	Sequence 60, App
161	2.1	1.8	1502	US-09-206-903A-2	Sequence 2, App	234	20	1.7	177	2	US-08-849-701-6	Sequence 6, App
162	2.1	1.8	1502	US-09-206-903A-2	Sequence 2, App	235	20	1.7	232	2	US-08-619-542B-28	Sequence 28, App
163	2.1	1.8	1502	US-09-202-122-2	Sequence 2, App	236	20	1.7	232	4	US-09-191-136-29	Sequence 29, App
164	2.1	1.8	1502	US-09-202-122-2	Sequence 2, App	237	20	1.7	260	3	US-08-688-988-19	Sequence 19, App
165	2.1	1.8	1502	US-09-206-935-2	Sequence 2, App	238	20	1.7	280	1	US-08-849-701-7	Sequence 7, App
166	2.1	1.8	1502	US-09-206-935-3	Sequence 3, App	239	20	1.7	288	1	US-07-807-529A-38	Sequence 38, App
167	2.1	1.8	1502	US-09-206-936-2	Sequence 2, App	240	20	1.7	288	3	US-08-430-944D-102	Sequence 102, App
168	2.1	1.8	1502	US-09-206-936-3	Sequence 3, App	241	20	1.7	288	3	US-08-431-184-102	Sequence 102, App
169	2.1	1.8	1503	US-08-715-325-1	Sequence 1, App	242	20	1.7	310	1	US-08-702-344-10	Sequence 10, App
170	2.1	1.8	1558	US-08-416-870C-9	Sequence 9, App	243	20	1.7	320	1	US-08-629-939-5	Sequence 5, App
171	2.1	1.8	1619	US-08-208-007A-1	Sequence 1, App	244	20	1.7	320	1	US-08-759-873-5	Sequence 5, App
172	2.1	1.8	1619	PCT-US94-04781-1	Sequence 1, App	245	20	1.7	321	4	US-09-385-982-366	Sequence 366, App
173	2.1	1.8	1639	US-08-737-524B-1	Sequence 1, App	246	20	1.7	321	4	US-09-385-982-366	Sequence 366, App

c 247	20	1.7	349	4	US-09-385-982-22	Sequence 22, Appl	320	20	1.7	783	2	US-08-457-364-34	Sequence 34, Appl
248	20	1.7	358	4	US-08-991-789A-168	Sequence 168, App	321	20	1.7	783	2	US-08-456-262-34	Sequence 34, Appl
249	20	1.7	370	1	US-08-330-535A-25	Sequence 25, Appl	322	20	1.7	783	2	US-08-456-240-34	Sequence 34, Appl
250	20	1.7	370	1	US-08-688-145-7	Sequence 7, Appl	323	20	1.7	783	2	US-08-455-736-34	Sequence 34, Appl
251	20	1.7	370	2	US-08-838-844-25	Sequence 25, Appl	324	20	1.7	783	2	US-08-971-217-34	Sequence 34, Appl
252	20	1.7	371	1	US-08-664-596B-25	Sequence 25, Appl	325	20	1.7	783	2	US-09-350-600-34	Sequence 34, Appl
253	20	1.7	371	2	US-08-739-775-3	Sequence 3, Appl	326	20	1.7	807	2	US-08-531-927B-9	Sequence 9, Appl
254	20	1.7	377	2	US-08-454-557C-37	Sequence 37, Appl	327	20	1.7	836	2	US-08-837-029-1	Sequence 1, Appl
255	20	1.7	377	2	US-08-340-426D-37	Sequence 37, Appl	328	20	1.7	836	2	US-08-967-364-4	Sequence 4, Appl
256	20	1.7	377	2	US-08-450-673C-37	Sequence 37, Appl	329	20	1.7	836	2	US-09-368-408-4	Sequence 2, Appl
257	20	1.7	377	5	PCT-US95-17111A-37	Sequence 37, Appl	330	20	1.7	836	2	US-08-831-570-2	Sequence 2, Appl
258	20	1.7	380	1	US-08-126-587C-5	Sequence 5, Appl	331	20	1.7	863	3	US-08-943-731-171	Sequence 171, App
259	20	1.7	390	1	US-08-661-168-7	Sequence 7, Appl	332	20	1.7	863	3	US-08-889-502-20	Sequence 20, Appl
260	20	1.7	423	3	US-08-943-731-131	Sequence 131, App	333	20	1.7	880	4	US-09-247-373B-39	Sequence 39, Appl
261	20	1.7	433	1	US-07-987-272A-13	Sequence 13, Appl	334	20	1.7	890	4	US-09-475-516A-34	Sequence 34, Appl
262	20	1.7	447	4	US-09-370-253-15	Sequence 15, Appl	335	20	1.7	903	5	PCT-US95-06406A-21	Sequence 21, Appl
263	20	1.7	469	1	US-08-468-347-23	Sequence 23, Appl	336	20	1.7	905	5	PCT-US96-07709-24	Sequence 24, Appl
264	20	1.7	469	1	US-08-226-284-25	Sequence 25, Appl	337	20	1.7	905	5	PCT-US96-07709-26	Sequence 26, Appl
265	20	1.7	469	1	US-08-467-389-23	Sequence 23, Appl	338	20	1.7	925	1	US-07-990-301A-3	Sequence 3, Appl
266	20	1.7	469	2	US-08-779-379-23	Sequence 23, Appl	339	20	1.7	932	3	US-08-906-616-88	Sequence 88, Appl
267	20	1.7	469	2	US-08-469-219-23	Sequence 23, Appl	340	20	1.7	932	3	US-08-817-795-88	Sequence 88, Appl
268	20	1.7	469	4	US-09-228-152-23	Sequence 23, Appl	341	20	1.7	932	3	US-08-639-075A-88	Sequence 88, Appl
269	20	1.7	522	1	US-08-289-247B-1	Sequence 1, Appl	342	20	1.7	932	3	US-09-012-431-88	Sequence 31, Appl
270	20	1.7	522	5	PCT-US95-09762-1	Sequence 1, Appl	343	20	1.7	932	4	US-09-032-215-33	Sequence 33, Appl
271	20	1.7	523	4	US-09-385-982-188	Sequence 188, App	344	20	1.7	932	4	US-09-012-692-88	Sequence 88, Appl
272	20	1.7	530	3	US-08-758-662-4	Sequence 4, Appl	345	20	1.7	932	4	US-08-906-613-88	Sequence 88, Appl
273	20	1.7	530	3	US-08-758-662-4	Sequence 4, Appl	346	20	1.7	932	4	US-08-906-613-88	Sequence 88, Appl
274	20	1.7	571	2	US-08-803-899-1	Sequence 1, Appl	347	20	1.7	932	5	PCT-US95-14442A-88	Sequence 37, Appl
275	20	1.7	571	2	US-08-803-899-1	Sequence 1, Appl	348	20	1.7	932	5	PCT-US95-14442A-88	Sequence 37, Appl
c 275	20	1.7	581	4	US-09-020-956-103	Sequence 103, App	349	20	1.7	932	5	PCT-US95-14442A-88	Sequence 37, Appl
276	20	1.7	581	4	US-09-030-607-103	Sequence 103, App	350	20	1.7	932	5	PCT-US95-14442A-88	Sequence 37, Appl
277	20	1.7	582	4	US-09-328-111-569	Sequence 569, App	351	20	1.7	945	4	US-09-248-335-37	Sequence 3, Appl
278	20	1.7	582	4	US-09-030-607-203	Sequence 203, App	352	20	1.7	965	4	US-09-268-364-3	Sequence 1, Appl
c 278	20	1.7	588	4	US-09-385-982-128	Sequence 128, App	353	20	1.7	972	1	US-09-141-135-1	Sequence 1, Appl
280	20	1.7	591	4	US-09-385-982-289	Sequence 289, App	354	20	1.7	972	1	US-07-915-934-1	Sequence 1, Appl
c 280	20	1.7	591	4	US-08-539-304A-1	Sequence 1, Appl	355	20	1.7	972	1	US-08-325-743-1	Sequence 1, Appl
c 281	20	1.7	615	4	US-09-385-982-528	Sequence 528, App	356	20	1.7	972	1	US-08-330-535A-24	Sequence 24, Appl
c 282	20	1.7	615	4	US-09-385-982-528	Sequence 528, App	357	20	1.7	972	2	US-08-838-844-24	Sequence 24, Appl
c 283	20	1.7	618	4	US-09-385-982-218	Sequence 218, App	358	20	1.7	989	2	US-08-874-460-1	Sequence 1, Appl
c 284	20	1.7	619	4	US-09-385-982-338	Sequence 338, App	359	20	1.7	1000	4	US-09-018-584A-33	Sequence 33, Appl
285	20	1.7	623	4	US-09-385-982-512	Sequence 512, App	360	20	1.7	1000	4	US-09-018-584A-34	Sequence 34, Appl
c 285	20	1.7	627	4	US-09-385-982-4	Sequence 4, Appl	361	20	1.7	1000	4	US-09-357-251-19	Sequence 19, Appl
c 286	20	1.7	627	4	US-09-385-982-4	Sequence 4, Appl	362	20	1.7	1001	1	US-08-728-259A-10	Sequence 10, Appl
c 287	20	1.7	640	4	US-09-385-982-2	Sequence 2, Appl	363	20	1.7	1001	2	US-08-473-486-10	Sequence 10, Appl
c 288	20	1.7	644	4	US-09-328-111-299	Sequence 299, App	364	20	1.7	1026	2	US-08-975-316-6	Sequence 6, Appl
c 289	20	1.7	645	4	US-09-328-111-106	Sequence 106, App	365	20	1.7	1026	2	US-08-975-316-6	Sequence 6, Appl
c 290	20	1.7	645	4	US-09-385-982-40	Sequence 40, Appl	366	20	1.7	1026	2	US-08-975-316-6	Sequence 6, Appl
c 291	20	1.7	646	4	US-09-385-982-314	Sequence 314, App	367	20	1.7	1041	2	US-08-580-545B-5	Sequence 5, Appl
c 292	20	1.7	648	4	US-09-385-982-332	Sequence 332, App	368	20	1.7	1041	2	US-08-580-545B-5	Sequence 5, Appl
c 293	20	1.7	650	4	US-09-328-111-179	Sequence 179, App	369	20	1.7	1041	2	US-08-580-545B-5	Sequence 5, Appl
c 294	20	1.7	653	4	US-09-385-982-324	Sequence 324, App	370	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 295	20	1.7	653	4	US-09-003-574-20	Sequence 20, App	371	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 296	20	1.7	689	4	US-09-003-574-20	Sequence 20, App	372	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 297	20	1.7	689	4	US-09-003-574-20	Sequence 20, App	373	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 298	20	1.7	697	1	US-08-468-347-25	Sequence 25, App	374	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 299	20	1.7	697	2	US-08-467-389-25	Sequence 25, App	375	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 300	20	1.7	697	2	US-08-779-379-25	Sequence 25, App	376	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 301	20	1.7	697	2	US-08-469-219-25	Sequence 25, App	377	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 302	20	1.7	703	4	US-09-328-152-25	Sequence 25, App	378	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 303	20	1.7	729	1	US-08-313-300-6	Sequence 6, Appl	379	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 304	20	1.7	731	1	US-08-447-010-1	Sequence 1, Appl	380	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 305	20	1.7	731	1	US-08-451-405A-2	Sequence 2, Appl	381	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 306	20	1.7	739	1	US-08-363-010-3	Sequence 3, Appl	382	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 307	20	1.7	739	1	US-08-363-010-3	Sequence 3, Appl	383	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 308	20	1.7	775	1	US-08-376-157B-3	Sequence 3, Appl	384	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 309	20	1.7	775	4	US-09-004-731-11	Sequence 11, Appl	385	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 310	20	1.7	775	4	US-08-749-699-9	Sequence 9, Appl	386	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 311	20	1.7	775	4	US-08-749-699-9	Sequence 9, Appl	387	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 312	20	1.7	775	5	PCT-US96-00845-3	Sequence 3, Appl	388	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 313	20	1.7	783	1	US-08-181-271A-34	Sequence 34, Appl	389	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 314	20	1.7	783	1	US-08-449-315-34	Sequence 34, Appl	390	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 315	20	1.7	783	1	US-08-444-803-34	Sequence 34, Appl	391	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 316	20	1.7	783	1	US-08-449-043-34	Sequence 34, Appl	392	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 317	20	1.7	783	1	US-08-456-265A-34	Sequence 34, Appl	393	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 318	20	1.7	783	1	US-08-455-416-34	Sequence 34, Appl	394	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 319	20	1.7	783	1	US-08-455-244-34	Sequence 34, Appl	395	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 320	20	1.7	783	1	US-08-454-876-34	Sequence 34, Appl	396	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 321	20	1.7	783	1	US-08-454-876-34	Sequence 34, Appl	397	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 322	20	1.7	783	1	US-08-454-876-34	Sequence 34, Appl	398	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 323	20	1.7	783	1	US-08-454-876-34	Sequence 34, Appl	399	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 324	20	1.7	783	1	US-08-454-876-34	Sequence 34, Appl	400	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 325	20	1.7	783	1	US-08-454-876-34	Sequence 34, Appl	401	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 326	20	1.7	783	1	US-08-454-876-34	Sequence 34, Appl	402	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 327	20	1.7	783	1	US-08-454-876-34	Sequence 34, Appl	403	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 328	20	1.7	783	1	US-08-454-876-34	Sequence 34, Appl	404	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 329	20	1.7	783	1	US-08-454-876-34	Sequence 34, Appl	405	20	1.7	1055	3	US-08-702-344-18	Sequence 18, Appl
c 330	20	1.7	783	1	US-08-454-876-34	Sequence 34, Appl	406	20	1.7	1055	3	US-0	

393	20	1.7	1174	2	US-08-485-862B-39	Sequence 39, Appl	466	20	1.7	1480	2	US-08-450-673C-38	Sequence 38, Appl
394	20	1.7	1174	3	US-08-787-739-39	Sequence 39, Appl	467	20	1.7	1480	5	PCT-US95-17111A-38	Sequence 38, Appl
395	20	1.7	1174	3	US-08-487-077A-39	Sequence 39, Appl	468	20	1.7	1485	1	US-08-471-601-23	Sequence 23, Appl
396	20	1.7	1174	3	US-08-485-863A-39	Sequence 39, Appl	469	20	1.7	1485	1	US-08-474-556-23	Sequence 23, Appl
397	20	1.7	1174	4	US-08-485-049D-39	Sequence 39, Appl	470	20	1.7	1485	1	US-08-479-382-23	Sequence 23, Appl
398	20	1.7	1174	4	US-09-178-115-39	Sequence 39, Appl	471	20	1.7	1485	1	US-08-470-354-23	Sequence 23, Appl
399	20	1.7	1174	4	US-09-177-776-39	Sequence 39, Appl	472	20	1.7	1485	1	US-08-479-383-23	Sequence 23, Appl
400	20	1.7	1189	4	US-09-147-779A-7	Sequence 7, Appl	473	20	1.7	1485	2	US-08-479-041-23	Sequence 23, Appl
401	20	1.7	1191	2	US-08-671-320-14	Sequence 14, Appl	474	20	1.7	1485	4	US-08-819-646-23	Sequence 23, Appl
402	20	1.7	1191	2	US-08-671-320-14	Sequence 14, Appl	475	20	1.7	1500	1	US-08-487-037-4	Sequence 4, Appl
403	20	1.7	1193	1	US-08-036-555B-134	Sequence 134, App	476	20	1.7	1501	4	US-09-196-520-1	Sequence 1, Appl
404	20	1.7	1193	1	US-08-469-569-134	Sequence 134, App	477	20	1.7	1505	3	US-08-909-965C-13	Sequence 13, Appl
405	20	1.7	1193	1	US-08-249-322A-134	Sequence 134, App	478	20	1.7	1536	2	US-08-993-359-29	Sequence 29, Appl
406	20	1.7	1193	1	US-08-469-526A-134	Sequence 134, App	479	20	1.7	1576	4	US-09-282-305-9	Sequence 9, Appl
407	20	1.7	1193	2	US-08-734-591A-134	Sequence 134, App	480	20	1.7	1581	4	US-09-313-300-1	Sequence 1, Appl
408	20	1.7	1193	2	US-08-469-660-134	Sequence 134, App	481	20	1.7	1587	3	US-09-108-020-11	Sequence 11, Appl
409	20	1.7	1193	3	US-08-341-018-3	Sequence 3, Appl	482	20	1.7	1596	4	US-09-146-950-17	Sequence 17, Appl
410	20	1.7	1193	3	US-08-470-335-134	Sequence 134, App	483	20	1.7	1602	4	US-08-530-950-3	Sequence 3, Appl
411	20	1.7	1193	4	US-08-735-021-134	Sequence 134, App	484	20	1.7	1602	3	US-08-888-429A-3	Sequence 3, Appl
412	20	1.7	1193	4	US-08-734-664A-134	Sequence 134, App	485	20	1.7	1602	4	US-09-149-879-3	Sequence 3, Appl
413	20	1.7	1193	4	US-08-470-339-134	Sequence 134, App	486	20	1.7	1616	4	US-09-370-253-11	Sequence 11, Appl
414	20	1.7	1193	5	PCT-US94-05083C-130	Sequence 130, App	487	20	1.7	1622	4	US-09-334-601-9	Sequence 9, Appl
415	20	1.7	1193	5	PCT-US95-06846A-134	Sequence 134, App	488	20	1.7	1624	2	US-08-852-807-10	Sequence 10, Appl
416	20	1.7	1196	3	US-07-959-509-4	Sequence 4, Appl	489	20	1.7	1624	4	US-08-430-225A-19	Sequence 19, Appl
417	20	1.7	1207	3	US-08-166-412-1	Sequence 1, Appl	490	20	1.7	1628	2	US-08-883-515-3	Sequence 3, Appl
418	20	1.7	1228	3	US-08-826-246-9	Sequence 9, Appl	491	20	1.7	1664	1	US-07-250-740-34	Sequence 34, Appl
419	20	1.7	1228	3	US-08-944-495-9	Sequence 9, Appl	492	20	1.7	1664	1	US-07-695-472B-3	Sequence 3, Appl
420	20	1.7	1228	3	US-09-126-640-5	Sequence 5, Appl	493	20	1.7	1689	4	US-09-061-702-3	Sequence 3, Appl
421	20	1.7	1228	4	US-08-925-588-9	Sequence 9, Appl	494	20	1.7	1706	1	US-07-906-871-11	Sequence 11, Appl
422	20	1.7	1242	2	US-08-909-965C-5	Sequence 5, Appl	495	20	1.7	1711	1	US-08-568-147B-1	Sequence 1, Appl
423	20	1.7	1260	4	US-08-943-731-169	Sequence 169, App	496	20	1.7	1712	3	US-09-033-055A-12	Sequence 12, Appl
424	20	1.7	1269	1	US-08-212-190A-1	Sequence 1, Appl	497	20	1.7	1724	4	US-08-509-024-1	Sequence 1, Appl
425	20	1.7	1269	2	US-08-900-321-1	Sequence 1, Appl	498	20	1.7	1724	4	US-09-333-279-1	Sequence 1, Appl
426	20	1.7	1269	5	PCT-US95-03610-1	Sequence 1, Appl	499	20	1.7	1724	5	PCT-US96-12374-1	Sequence 1, Appl
427	20	1.7	1275	3	US-08-725-532A-2	Sequence 2, Appl	500	20	1.7	1736	4	US-09-360-197-13	Sequence 13, Appl
428	20	1.7	1275	3	US-08-909-965C-4	Sequence 4, Appl	501	20	1.7	1737	4	US-09-416-050A-7	Sequence 7, Appl
429	20	1.7	1278	1	US-08-463-262A-1	Sequence 1, Appl	502	20	1.7	1737	4	US-09-664-800-7	Sequence 7, Appl
430	20	1.7	1299	1	US-08-463-989-1	Sequence 1, Appl	503	20	1.7	1737	4	US-09-665-309-7	Sequence 7, Appl
431	20	1.7	1299	4	US-09-003-574-1	Sequence 1, Appl	504	20	1.7	1737	4	US-09-661-569-7	Sequence 7, Appl
432	20	1.7	1299	4	US-09-003-570-1	Sequence 1, Appl	505	20	1.7	1737	4	US-08-565-655-5	Sequence 5, Appl
433	20	1.7	1313	3	US-09-035-648-22	Sequence 22, Appl	506	20	1.7	1741	1	US-08-726-525-5	Sequence 5, Appl
434	20	1.7	1313	4	US-09-001-951-22	Sequence 22, Appl	507	20	1.7	1759	1	US-08-487-942-5	Sequence 5, Appl
435	20	1.7	1332	4	US-09-333-423-1	Sequence 1, Appl	508	20	1.7	1759	2	US-08-726-036A-5	Sequence 5, Appl
436	20	1.7	1334	2	US-08-481-658B-44	Sequence 44, Appl	509	20	1.7	1759	2	US-08-102-420B-15	Sequence 15, Appl
437	20	1.7	1334	2	US-08-477-504B-44	Sequence 44, Appl	510	20	1.7	1776	2	US-08-531-927B-1	Sequence 1, Appl
438	20	1.7	1334	2	US-08-486-756A-44	Sequence 44, Appl	511	20	1.7	1776	2	US-09-083-516-5	Sequence 5, Appl
439	20	1.7	1334	2	US-08-485-862B-44	Sequence 44, Appl	512	20	1.7	1776	4	US-09-041-886-12	Sequence 12, Appl
440	20	1.7	1334	3	US-08-787-739-44	Sequence 44, Appl	513	20	1.7	1784	3	US-08-991-426-1	Sequence 1, Appl
441	20	1.7	1334	3	US-08-487-077A-44	Sequence 44, Appl	514	20	1.7	1784	3	US-09-143-470-1	Sequence 1, Appl
442	20	1.7	1334	3	US-08-485-863A-44	Sequence 44, Appl	515	20	1.7	1817	3	US-08-564-486C-14	Sequence 14, Appl
443	20	1.7	1334	4	US-08-485-049D-44	Sequence 44, Appl	516	20	1.7	1821	4	US-09-056-105-23	Sequence 23, Appl
444	20	1.7	1334	4	US-08-485-115-44	Sequence 44, Appl	517	20	1.7	1826	2	US-08-808-931-15	Sequence 15, Appl
445	20	1.7	1334	4	US-09-177-776-44	Sequence 44, Appl	518	20	1.7	1826	3	US-08-808-323-15	Sequence 15, Appl
446	20	1.7	1342	2	US-08-909-965C-6	Sequence 6, Appl	519	20	1.7	1826	3	US-09-050-603A-15	Sequence 15, Appl
447	20	1.7	1347	4	US-09-140-804-1	Sequence 1, Appl	520	20	1.7	1833	6	5166195-1	Patent No. 5166195
448	20	1.7	1364	2	US-08-815-718-1	Sequence 1, Appl	521	20	1.7	1837	2	US-08-909-965C-10	Sequence 10, Appl
449	20	1.7	1368	3	US-08-707-399B-1	Sequence 1, Appl	522	20	1.7	1867	4	US-08-943-731-111	Sequence 111, App
450	20	1.7	1377	4	US-08-810-572A-1	Sequence 1, Appl	523	20	1.7	1875	2	US-08-683-743-3	Sequence 3, Appl
451	20	1.7	1384	4	US-08-729-594A-33	Sequence 33, Appl	524	20	1.7	1889	3	US-08-861-747-3	Sequence 3, Appl
452	20	1.7	1392	1	US-08-957-351-1	Sequence 1, Appl	525	20	1.7	1896	1	US-08-253-503-1	Sequence 1, Appl
453	20	1.7	1393	1	US-08-052-205-2	Sequence 2, Appl	526	20	1.7	1896	1	US-08-796-883-1	Sequence 1, Appl
454	20	1.7	1393	1	US-08-595-974-2	Sequence 2, Appl	527	20	1.7	1896	2	US-08-611-273B-1	Sequence 1, Appl
455	20	1.7	1395	2	US-08-553-367A-1	Sequence 1, Appl	528	20	1.7	1896	2	US-08-531-864-1	Sequence 1, Appl
456	20	1.7	1395	4	US-09-295-306-1	Sequence 14, Appl	529	20	1.7	1896	2	US-08-373-636C-1	Sequence 1, Appl
457	20	1.7	1410	5	PCT-US95-15428-14	Sequence 63, Appl	530	20	1.7	1896	2	US-08-602-506A-1	Sequence 1, Appl
458	20	1.7	1441	4	US-08-821-994-63	Sequence 174, App	531	20	1.7	1896	3	US-09-266-294-1	Sequence 1, Appl
459	20	1.7	1459	4	US-09-020-956-174	Sequence 174, App	532	20	1.7	1896	4	US-09-179-281-1	Sequence 1, Appl
460	20	1.7	1459	4	US-09-030-607-174	Sequence 3, Appl	533	20	1.7	1896	4	US-09-056-105-25	Sequence 25, Appl
461	20	1.7	1470	1	US-08-052-205-3	Sequence 3, Appl	534	20	1.7	1901	5	PCT-US93-05000-32	Sequence 32, Appl
462	20	1.7	1470	1	US-08-595-974-3	Sequence 1, Appl	535	20	1.7	1901	3	US-08-826-611-1	Sequence 1, Appl
463	20	1.7	1476	2	US-08-872-302-1	Sequence 38, Appl	536	20	1.7	1929	4	US-09-146-950-1	Sequence 1, Appl
464	20	1.7	1480	2	US-08-454-557C-38	Sequence 38, Appl	537	20	1.7	1933	3	US-08-627-907A-1	Sequence 1, Appl
465	20	1.7	1480	2	US-08-340-426D-38	Sequence 38, Appl	538	20	1.7	1933	3		

539	20	1.7	1952	1	US-08-333-358-1	Sequence 1, Appl	612	20	1.7	2729	1	US-07-938-782A-1	Sequence 1, Appl
540	20	1.7	1952	1	US-08-463-694-1	Sequence 1, Appl	613	20	1.7	2729	1	US-08-630-524-1	Sequence 1, Appl
541	20	1.7	1952	1	US-08-694-501-1	Sequence 1, Appl	614	20	1.7	2729	5	PCT-US93-08131-1	Sequence 1, Appl
542	20	1.7	1957	4	US-09-352-990-11	Sequence 11, Appl	615	20	1.7	2834	1	US-08-276-151-8	Sequence 8, Appl
543	20	1.7	1969	2	US-08-541-033A-7	Sequence 7, Appl	616	20	1.7	2886	2	US-08-687-080-55	Sequence 55, Appl
544	20	1.7	1969	2	US-08-828-451-7	Sequence 7, Appl	617	20	1.7	2923	1	US-08-480-449-1	Sequence 1, Appl
545	20	1.7	1977	2	US-08-574-959A-3	Sequence 3, Appl	618	20	1.7	2923	2	US-08-660-542-1	Sequence 5, Appl
546	20	1.7	1977	4	US-09-357-014-3	Sequence 3, Appl	619	20	1.7	2923	4	US-09-232-878-5	Sequence 5, Appl
547	20	1.7	1977	4	US-07-937-609-25	Sequence 25, Appl	620	20	1.7	2927	4	US-08-716-873-12	Sequence 12, Appl
548	20	1.7	2015	4	US-08-029-170-25	Sequence 25, Appl	621	20	1.7	2935	4	US-09-368-431-12	Sequence 12, Appl
549	20	1.7	2017	4	US-08-436-583-1	Sequence 1, Appl	622	20	1.7	2935	4	US-07-688-352C-31	Sequence 31, Appl
550	20	1.7	2022	2	US-08-464-517-32	Sequence 32, Appl	623	20	1.7	3073	1	US-08-474-379C-31	Sequence 31, Appl
551	20	1.7	2022	2	US-08-246-361A-32	Sequence 32, Appl	624	20	1.7	3073	2	US-08-474-379C-31	Sequence 31, Appl
552	20	1.7	2022	3	US-08-463-772-32	Sequence 32, Appl	625	20	1.7	3073	3	US-09-146-249A-31	Sequence 31, Appl
553	20	1.7	2026	1	US-08-503-133A-1	Sequence 1, Appl	626	20	1.7	3073	3	US-08-206-188B-31	Sequence 31, Appl
554	20	1.7	2026	2	US-08-576-775A-1	Sequence 1, Appl	627	20	1.7	3113	5	PCT-US91-0271A-30	Sequence 20, Appl
555	20	1.7	2026	2	US-08-972-498-1	Sequence 1, Appl	628	20	1.7	3141	2	US-08-993-228-20	Sequence 20, Appl
556	20	1.7	2026	3	US-08-899-545-1	Sequence 1, Appl	629	20	1.7	3141	3	US-08-956-242-1	Sequence 1, Appl
557	20	1.7	2034	1	US-08-559-492-2	Sequence 2, Appl	630	20	1.7	3158	2	US-09-351-215-1	Sequence 1, Appl
558	20	1.7	2048	1	US-07-602-608-11	Sequence 11, Appl	631	20	1.7	3158	2	US-08-464-517-36	Sequence 36, Appl
559	20	1.7	2048	1	US-08-261-578-11	Sequence 11, Appl	632	20	1.7	3158	3	US-08-463-772-36	Sequence 36, Appl
560	20	1.7	2059	1	US-08-256-130A-2	Sequence 2, Appl	633	20	1.7	3212	4	US-08-697-954-1	Sequence 1, Appl
561	20	1.7	2082	2	US-08-785-310A-2	Sequence 2, Appl	634	20	1.7	3238	4	US-08-123-934A-5	Sequence 5, Appl
562	20	1.7	2096	2	US-08-541-033A-19	Sequence 19, Appl	635	20	1.7	3238	5	PCT-US94-10080-5	Sequence 5, Appl
563	20	1.7	2096	2	US-08-828-451-19	Sequence 19, Appl	636	20	1.7	3350	1	US-08-247-946A-2	Sequence 2, Appl
564	20	1.7	2099	2	US-08-541-033A-3	Sequence 3, Appl	637	20	1.7	3350	3	US-09-110-116-2	Sequence 2, Appl
565	20	1.7	2099	4	US-08-828-451-3	Sequence 3, Appl	638	20	1.7	3350	5	PCT-US95-06420-2	Sequence 2, Appl
566	20	1.7	2099	4	US-08-938-669A-5	Sequence 5, Appl	639	20	1.7	3507	1	US-08-832-883-67	Sequence 67, Appl
567	20	1.7	2103	2	US-08-897-340-2	Sequence 2, Appl	640	20	1.7	3507	2	US-08-832-877-67	Sequence 67, Appl
568	20	1.7	2103	3	US-09-252-329-2	Sequence 2, Appl	641	20	1.7	3566	4	US-09-086-483A-1	Sequence 1, Appl
569	20	1.7	2119	2	US-08-381-691-17	Sequence 17, Appl	642	20	1.7	3566	4	US-08-362-670B-9	Sequence 9, Appl
570	20	1.7	2137	2	US-08-541-033A-18	Sequence 18, Appl	643	20	1.7	3585	3	US-08-333-576C-9	Sequence 9, Appl
571	20	1.7	2137	2	US-08-828-451-18	Sequence 18, Appl	644	20	1.7	3585	3	US-08-808-324-9	Sequence 9, Appl
572	20	1.7	2140	2	US-08-541-033A-1	Sequence 1, Appl	645	20	1.7	3585	5	PCT-US94-14030A-9	Sequence 4, Appl
573	20	1.7	2140	2	US-08-828-451-1	Sequence 1, Appl	646	20	1.7	3597	4	US-09-095-758-4	Sequence 4, Appl
574	20	1.7	2141	1	US-08-463-931-1	Sequence 1, Appl	647	20	1.7	3597	4	US-09-422-968-4	Sequence 4, Appl
575	20	1.7	2158	1	US-07-602-608-1	Sequence 1, Appl	648	20	1.7	3607	2	US-08-629-001A-8	Sequence 8, Appl
576	20	1.7	2158	1	US-08-261-578-1	Sequence 1, Appl	649	20	1.7	3607	4	US-08-642-274D-8	Sequence 8, Appl
577	20	1.7	2198	2	US-08-755-728-2	Sequence 2, Appl	650	20	1.7	3607	4	US-08-952-127-8	Sequence 8, Appl
578	20	1.7	2198	2	US-08-974-655-2	Sequence 2, Appl	651	20	1.7	3607	4	US-08-952-014C-8	Sequence 8, Appl
579	20	1.7	2198	4	US-09-283-011-2	Sequence 1, Appl	652	20	1.7	3692	2	US-08-588-983-17	Sequence 17, Appl
580	20	1.7	2226	3	US-08-951-260A-1	Sequence 3, Appl	653	20	1.7	3692	2	US-08-588-976-17	Sequence 17, Appl
581	20	1.7	2309	3	US-09-078-317-3	Sequence 3, Appl	654	20	1.7	3742	1	US-08-694-915-5	Sequence 5, Appl
582	20	1.7	2313	3	US-08-738-168B-14	Sequence 14, Appl	655	20	1.7	3742	1	US-08-185-432-3	Sequence 3, Appl
583	20	1.7	2335	3	US-09-387-574-9	Sequence 9, Appl	656	20	1.7	3771	1	US-08-185-432-3	Sequence 3, Appl
584	20	1.7	2343	3	US-09-031-392-1	Sequence 1, Appl	657	20	1.7	3771	1	US-09-112-096-28	Sequence 28, Appl
585	20	1.7	2343	3	US-09-299-549-1	Sequence 1, Appl	658	20	1.7	3848	4	US-08-185-432-3	Sequence 81, Appl
586	20	1.7	2351	1	US-08-168-091A-1	Sequence 1, Appl	659	20	1.7	3867	4	US-09-347-114A-81	Sequence 1, Appl
587	20	1.7	2362	1	US-08-265-087-1	Sequence 1, Appl	660	20	1.7	3885	1	US-08-688-145-1	Sequence 1, Appl
588	20	1.7	2362	1	US-08-621-493-1	Sequence 1, Appl	661	20	1.7	3946	3	US-09-083-351-1	Sequence 1, Appl
589	20	1.7	2362	2	US-08-965-688-1	Sequence 1, Appl	662	20	1.7	3946	4	US-09-083-352-1	Sequence 16, Appl
590	20	1.7	2362	2	US-08-965-688-1	Sequence 1, Appl	663	20	1.7	3952	2	US-08-381-691-16	Sequence 8, Appl
591	20	1.7	2380	5	PCT-US95-16980-2	Sequence 2, Appl	664	20	1.7	4032	1	US-08-126-587C-8	Sequence 17, Appl
592	20	1.7	2381	1	US-08-021-608D-9	Sequence 9, Appl	665	20	1.7	4032	4	US-08-406-030A-17	Sequence 4, Appl
593	20	1.7	2381	5	PCT-US94-01782-9	Sequence 9, Appl	666	20	1.7	4131	1	US-08-485-588-4	Sequence 4, Appl
594	20	1.7	2381	5	US-09-260-173-1	Sequence 1, Appl	667	20	1.7	4131	1	US-08-484-565-4	Sequence 4, Appl
595	20	1.7	2384	1	US-08-726-160-1	Sequence 1, Appl	668	20	1.7	4131	1	US-08-480-751-4	Sequence 4, Appl
596	20	1.7	2384	5	PCT-US94-01782-1	Sequence 1, Appl	669	20	1.7	4131	3	US-08-943-986-4	Sequence 4, Appl
597	20	1.7	2413	4	US-09-518-046-1	Sequence 4, Appl	670	20	1.7	4131	3	US-08-353-784-4	Sequence 4, Appl
598	20	1.7	2416	4	US-09-261-416-1	Sequence 1, Appl	671	20	1.7	4195	1	US-08-484-719B-4	Sequence 1, Appl
599	20	1.7	2420	5	PCT-US93-00227-1	Sequence 12, Appl	672	20	1.7	4326	2	US-08-200-016-1	Sequence 12, Appl
600	20	1.7	2447	4	US-08-387-707-12	Sequence 111, App	673	20	1.7	4326	3	US-08-852-807-12	Sequence 7, Appl
601	20	1.7	2448	2	US-08-687-080-111	Sequence 3, Appl	674	20	1.7	4337	3	US-09-187-049-1	Sequence 7, Appl
602	20	1.7	2544	4	US-09-518-046-3	Sequence 15, Appl	675	20	1.7	4524	3	US-08-845-998-7	Sequence 7, Appl
603	20	1.7	2555	2	US-08-960-022-15	Sequence 3, Appl	676	20	1.7	4524	3	US-09-206-537-7	Sequence 35, Appl
604	20	1.7	2555	2	US-08-326-286-3	Sequence 3, Appl	677	20	1.7	4524	4	US-09-430-854-7	Sequence 53, Appl
605	20	1.7	2587	2	US-08-326-286-3	Sequence 3, Appl	678	20	1.7	4550	4	US-09-103-663-35	Sequence 53, Appl
606	20	1.7	2589	6	5212286-1	Patent No. 5212286	679	20	1.7	4586	2	US-08-832-877-53	Sequence 53, Appl
607	20	1.7	2630	3	US-08-669-286-6	Sequence 6, Appl	680	20	1.7	4612	4	US-08-960-048-2	Sequence 2, Appl
608	20	1.7	2630	4	US-09-469-253-6	Sequence 6, Appl	681	20	1.7	4612	4	US-08-188-582-1	Sequence 1, Appl
609	20	1.7	2630	4	US-09-642-146-6	Sequence 6, Appl	682	20	1.7	4615	1	US-08-188-582-1	Sequence 1, Appl
610	20	1.7	2665	3	US-09-040-005-1	Sequence 1, Appl	683	20	1.7	4668	4	US-08-646-715-1	Sequence 1, Appl
611	20	1.7	2688	2	US-08-909-965C-1	Sequence 1, Appl	684	20	1.7	4671	4	US-09-042-437-27	Sequence 27, Appl

c 685	20	1.7	4741	1	US-07-695-472B-4	Sequence 4, Appli	c 758	20	1.7	10898	2	US-08-486-756A-5	Sequence 5, Appli
c 686	20	1.7	4742	1	US-08-250-740-35	Sequence 35, Appli	c 759	20	1.7	10898	2	US-08-485-862B-5	Sequence 5, Appli
c 687	20	1.7	4743	1	US-08-884-324-9	Sequence 9, Appli	c 760	20	1.7	10898	2	US-08-485-862B-5	Sequence 5, Appli
c 688	20	1.7	4843	3	US-08-986-485-1	Sequence 1, Appli	c 761	20	1.7	10898	3	US-08-787-739-5	Sequence 5, Appli
c 689	20	1.7	4978	1	US-08-220-603A-1	Sequence 1, Appli	c 762	20	1.7	10898	3	US-08-787-739-5	Sequence 5, Appli
c 690	20	1.7	5162	2	US-08-916-917-13	Sequence 13, Appli	c 763	20	1.7	10898	3	US-08-487-077A-5	Sequence 5, Appli
c 691	20	1.7	5162	3	US-09-225-170-13	Sequence 13, Appli	c 764	20	1.7	10898	3	US-08-487-077A-5	Sequence 5, Appli
c 692	20	1.7	5176	4	US-08-654-482-13	Sequence 13, Appli	c 765	20	1.7	10898	3	US-08-485-863A-5	Sequence 5, Appli
c 693	20	1.7	5232	4	US-08-972-927-13	Sequence 13, Appli	c 766	20	1.7	10898	3	US-08-485-863A-5	Sequence 5, Appli
c 694	20	1.7	5261	1	US-08-045-806-3	Sequence 1, Appli	c 767	20	1.7	10898	4	US-08-485-049D-5	Sequence 5, Appli
c 695	20	1.7	5261	1	US-08-368-051B-3	Sequence 3, Appli	c 768	20	1.7	10898	4	US-08-485-049D-5	Sequence 5, Appli
c 696	20	1.7	5375	3	US-08-757-223-7	Sequence 3, Appli	c 769	20	1.7	10898	4	US-09-178-115-5	Sequence 5, Appli
c 697	20	1.7	5499	1	US-07-695-564-4	Sequence 7, Appli	c 770	20	1.7	10898	4	US-09-177-776-5	Sequence 5, Appli
c 698	20	1.7	5499	1	US-08-241-387-4	Sequence 4, Appli	c 771	20	1.7	10898	4	US-09-177-776-5	Sequence 5, Appli
c 699	20	1.7	5590	4	US-09-050-159-129	Sequence 139, App	c 772	20	1.7	10898	4	US-09-177-776-5	Sequence 5, Appli
c 700	20	1.7	5629	1	US-07-695-564-2	Sequence 2, Appli	c 773	20	1.7	10898	4	US-07-869-933-31	Sequence 31, Appli
c 701	20	1.7	5629	1	US-08-241-387-2	Sequence 2, Appli	c 774	20	1.7	11298	1	US-07-869-933-31	Sequence 31, Appli
c 702	20	1.7	5668	4	US-09-112-096-14	Sequence 14, Appli	c 775	20	1.7	11298	1	US-08-201-879A-2	Sequence 2, Appli
c 703	20	1.7	5835	4	US-09-033-333-3	Sequence 3, Appli	c 776	20	1.7	11298	1	US-09-103-663-31	Sequence 31, Appli
c 704	20	1.7	5836	1	US-08-380-916-1	Sequence 1, Appli	c 777	20	1.7	11464	3	US-08-884-324-13	Sequence 13, Appli
c 705	20	1.7	5836	3	US-08-721-690-1	Sequence 1, Appli	c 778	20	1.7	11531	1	US-08-068-945A-1	Sequence 1, Appli
c 706	20	1.7	5836	3	US-08-891-581-1	Sequence 1, Appli	c 779	20	1.7	11531	1	US-08-442-806-1	Sequence 1, Appli
c 707	20	1.7	5836	1	US-08-033-333-2	Sequence 2, Appli	c 780	20	1.7	11613	1	US-08-484-044-10	Sequence 10, Appli
c 708	20	1.7	6063	1	US-08-135-744-4	Sequence 4, Appli	c 781	20	1.7	11811	4	US-09-078-294-7	Sequence 7, Appli
c 709	20	1.7	6063	2	US-08-788-279-4	Sequence 4, Appli	c 782	20	1.7	12047	2	US-09-022-461-1	Sequence 1, Appli
c 710	20	1.7	6354	3	US-09-058-389A-5	Sequence 5, Appli	c 783	20	1.7	13158	2	US-08-687-080-105	Sequence 105, App
c 711	20	1.7	6623	2	US-08-687-080-68	Sequence 68, Appli	c 784	20	1.7	13674	2	US-08-852-807-1	Sequence 1, Appli
c 712	20	1.7	6769	1	US-08-480-784-20	Sequence 20, Appli	c 785	20	1.7	13865	3	US-09-009-217-11	Sequence 11, Appli
c 713	20	1.7	6769	1	US-08-483-553-20	Sequence 20, Appli	c 786	20	1.7	13865	3	US-09-009-217-11	Sequence 11, Appli
c 714	20	1.7	6769	1	US-08-483-553-20	Sequence 20, Appli	c 787	20	1.7	14636	4	US-09-173-914-6	Sequence 6, Appli
c 715	20	1.7	6769	1	US-08-487-002-20	Sequence 20, Appli	c 788	20	1.7	15328	5	US-08-888-497-33	Sequence 33, Appli
c 716	20	1.7	6769	1	US-08-354B-20	Sequence 20, Appli	c 789	20	1.7	15328	5	PCT-US94-07926-33	Sequence 33, Appli
c 717	20	1.7	6769	1	US-08-488-011B-20	Sequence 20, Appli	c 790	20	1.7	17041	4	US-08-076-011-1	Sequence 1, Appli
c 718	20	1.7	6769	4	US-08-850-727-20	Sequence 20, Appli	c 791	20	1.7	17056	4	US-09-245-041-3	Sequence 3, Appli
c 719	20	1.7	6769	5	PCT-US95-10202-20	Sequence 20, Appli	c 792	20	1.7	17327	1	US-07-906-871-15	Sequence 15, Appli
c 720	20	1.7	6769	5	PCT-US95-10203-20	Sequence 20, Appli	c 793	20	1.7	17327	1	US-07-906-871-15	Sequence 15, Appli
c 721	20	1.7	7130	4	US-09-056-105-31	Sequence 31, Appli	c 794	20	1.7	17606	4	US-08-943-731-4	Sequence 4, Appli
c 722	20	1.7	7291	4	US-08-913-942-3	Sequence 3, Appli	c 795	20	1.7	17606	4	US-09-087-465-3	Sequence 3, Appli
c 723	20	1.7	8201	1	US-08-253-155A-9	Sequence 9, Appli	c 796	20	1.7	17949	4	US-09-087-465-3	Sequence 3, Appli
c 724	20	1.7	8342	3	US-08-545-860D-63	Sequence 63, Appli	c 797	20	1.7	17949	4	US-09-078-294-12	Sequence 12, Appli
c 725	20	1.7	8342	5	PCT-US94-04496-63	Sequence 63, Appli	c 798	20	1.7	18073	4	US-09-318-448-11	Sequence 11, Appli
c 726	20	1.7	8392	3	US-08-080-255-6	Sequence 6, Appli	c 799	20	1.7	18073	4	US-08-370-975B-6	Sequence 6, Appli
c 727	20	1.7	8392	3	US-08-465-713-6	Sequence 6, Appli	c 800	20	1.7	18596	4	PCT-US95-07201-43	Sequence 43, Appli
c 728	20	1.7	8392	5	PCT-US93-05857-6	Sequence 6, Appli	c 801	20	1.7	22481	5	US-08-469-461-3	Sequence 3, Appli
c 729	20	1.7	8453	3	US-09-167-681-45	Sequence 45, Appli	c 802	20	1.7	22846	3	US-07-890-609-3	Sequence 3, Appli
c 730	20	1.7	8517	3	US-08-827-208-1	Sequence 1, Appli	c 803	20	1.7	22846	3	US-08-943-731-3	Sequence 3, Appli
c 731	20	1.7	8517	4	US-09-500-358-1	Sequence 1, Appli	c 804	20	1.7	24183	4	US-08-943-731-3	Sequence 3, Appli
c 732	20	1.7	8517	4	US-09-498-809-1	Sequence 1, Appli	c 805	20	1.7	26764	1	US-08-370-975B-1	Sequence 1, Appli
c 733	20	1.7	9278	1	US-08-243-542-9	Sequence 9, Appli	c 806	20	1.7	26764	1	US-08-884-324-14	Sequence 14, Appli
c 734	20	1.7	9278	1	US-08-477-407-9	Sequence 9, Appli	c 807	20	1.7	28994	3	US-08-323-443B-1	Sequence 1, Appli
c 735	20	1.7	9278	1	US-08-484-355-9	Sequence 9, Appli	c 808	20	1.7	31571	1	US-08-323-443B-1	Sequence 1, Appli
c 736	20	1.7	9734	1	US-08-347-114A-80	Sequence 80, Appli	c 809	20	1.7	35100	5	US-08-306-691B-19	Sequence 19, Appli
c 737	20	1.7	9844	4	US-08-462-437-30	Sequence 30, Appli	c 810	20	1.7	35100	5	PCT-US93-06251-19	Sequence 19, Appli
c 738	20	1.7	10079	2	US-08-476-866-20	Sequence 20, Appli	c 811	20	1.7	36741	4	US-09-301-665-3	Sequence 3, Appli
c 739	20	1.7	10079	2	US-08-476-866-20	Sequence 20, Appli	c 812	20	1.7	36741	4	US-09-301-665-3	Sequence 3, Appli
c 740	20	1.7	10380	3	US-09-077-354B-3	Sequence 3, Appli	c 813	20	1.7	4328	3	US-08-742-185-102	Sequence 102, App
c 741	20	1.7	10825	4	US-08-652-265-1	Sequence 1, Appli	c 814	20	1.7	4328	3	US-08-742-185-102	Sequence 102, App
c 742	20	1.7	10825	3	US-08-652-265-3	Sequence 3, Appli	c 815	20	1.7	43795	3	US-08-742-185-101	Sequence 101, App
c 743	20	1.7	10825	3	US-08-652-265-5	Sequence 5, Appli	c 816	20	1.7	43795	3	US-08-742-185-101	Sequence 101, App
c 744	20	1.7	10825	3	US-08-652-265-7	Sequence 7, Appli	c 817	20	1.7	49136	4	US-09-422-869-1	Sequence 1, Appli
c 745	20	1.7	10825	3	US-08-834-497A-1	Sequence 1, Appli	c 818	20	1.7	53526	3	US-08-658-136-2	Sequence 2, Appli
c 746	20	1.7	10825	3	US-08-834-497A-3	Sequence 3, Appli	c 819	20	1.7	53526	3	US-08-658-136-2	Sequence 2, Appli
c 747	20	1.7	10825	3	US-08-834-497A-5	Sequence 5, Appli	c 820	20	1.7	53577	3	US-08-658-136-1	Sequence 1, Appli
c 748	20	1.7	10825	3	US-08-834-497A-7	Sequence 7, Appli	c 821	20	1.7	53577	3	US-08-658-136-1	Sequence 1, Appli
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c 750	20	1.7	10825	4	US-09-503-444A-3	Sequence 3, Appli	c 823	20	1.7	56516	2	US-09-338-907-1	Sequence 1, Appli
c 751	20	1.7	10825	4	US-09-503-444A-5	Sequence 5, Appli	c 824	20	1.7	56520	4	US-03-338-907-179	Sequence 179, App
c 752	20	1.7	10825	4	US-09-503-444A-7	Sequence 7, Appli	c 825	20	1.7	72928	3	US-09-009-913-1	Sequence 1, Appli
c 753	20	1.7	10898	2	US-08-481-658B-5	Sequence 5, Appli	c 826	20	1.7	72928	3	US-09-009-913-1	Sequence 1, Appli
c 754	20	1.7	10898	2	US-08-481-658B-5	Sequence 5, Appli	c 827	20	1.7	80246	4	US-09-078-294-4	Sequence 4, Appli
c 755	20	1.7	10898	2	US-08-477-504A-5	Sequence 5, Appli	c 828	20	1.7	80595	4	US-09-078-294-3	Sequence 3, Appli
c 756	20	1.7	10898	2	US-08-477-504A-5	Sequence 5, Appli	c 829	20	1.7	80595	4	US-09-078-294-3	Sequence 3, Appli
c 757	20	1.7	10898	2	US-08-486-756A-5	Sequence 5, Appli	c 830	20	1.7	87350	3	US-08-781-891-79	Sequence 79, Appli

831	20	1.7	152331	3	US-09-128-155-16	Sequence 16, Appl	c 904	19	1.6	56	2	US-08-776-944-9	Sequence 9, Appl
832	20	1.7	176373	3	US-09-128-155-17	Sequence 17, Appl	905	19	1.6	57	1	US-08-120-827-85	Sequence 85, Appl
c 833	20	1.7	176373	3	US-09-128-155-17	Sequence 17, Appl	906	19	1.6	57	1	US-08-120-827-93	Sequence 93, Appl
c 834	20	1.7	246240	2	US-08-724-394A-20	Sequence 20, Appl	c 907	19	1.6	57	1	US-08-323-084A-20	Sequence 20, Appl
c 835	20	1.7	246240	2	US-08-724-394A-21	Sequence 21, Appl	c 908	19	1.6	57	1	US-08-674-008-20	Sequence 20, Appl
c 836	20	1.7	246240	2	US-08-724-394A-22	Sequence 22, Appl	c 909	19	1.6	57	1	US-08-478-675-85	Sequence 85, Appl
c 837	19	1.6	20	4	US-08-482-918-32	Sequence 32, Appl	c 910	19	1.6	57	1	US-08-478-675-93	Sequence 93, Appl
c 838	19	1.6	20	4	US-09-224-681-32	Sequence 32, Appl	c 911	19	1.6	57	4	US-09-199-737-59	Sequence 59, Appl
c 839	19	1.6	20	4	US-08-336-728A-32	Sequence 32, Appl	c 912	19	1.6	59	4	US-09-443-501A-16	Sequence 16, Appl
c 840	19	1.6	23	5	PCT-US94-05407-7	Sequence 7, Appl	c 913	19	1.6	60	4	US-09-257-581-3	Sequence 3, Appl
c 841	19	1.6	23	5	PCT-US94-05407-8	Sequence 8, Appl	c 914	19	1.6	63	1	US-08-232-463-47	Sequence 47, Appl
c 842	19	1.6	25	1	US-08-113-646A-42	Sequence 42, Appl	c 915	19	1.6	69	4	US-09-265-911A-8	Sequence 8, Appl
c 843	19	1.6	26	1	US-08-621-914A-3	Sequence 3, Appl	c 916	19	1.6	70	2	US-08-097-554A-43	Sequence 43, Appl
c 844	19	1.6	30	1	US-08-455-627-12	Sequence 12, Appl	c 917	19	1.6	70	2	US-08-776-944-12	Sequence 12, Appl
c 845	19	1.6	30	1	US-08-480-784-41	Sequence 41, Appl	c 918	19	1.6	70	3	US-08-480-640A-43	Sequence 43, Appl
c 846	19	1.6	30	1	US-08-483-553-41	Sequence 41, Appl	c 919	19	1.6	70	3	US-08-295-802-43	Sequence 43, Appl
c 847	19	1.6	30	1	US-08-487-002-41	Sequence 41, Appl	c 920	19	1.6	70	4	US-08-488-237A-43	Sequence 43, Appl
c 848	19	1.6	30	1	US-08-483-554B-41	Sequence 41, Appl	c 921	19	1.6	74	2	US-08-097-554A-44	Sequence 44, Appl
c 849	19	1.6	30	1	US-08-488-011B-41	Sequence 41, Appl	c 922	19	1.6	74	3	US-08-480-640A-44	Sequence 44, Appl
c 850	19	1.6	30	2	US-08-689-856-12	Sequence 12, Appl	c 923	19	1.6	74	3	US-08-295-802-44	Sequence 44, Appl
c 851	19	1.6	30	4	US-08-850-727-41	Sequence 41, Appl	c 924	19	1.6	74	4	US-08-488-237A-44	Sequence 44, Appl
c 852	19	1.6	30	4	US-08-787-321-12	Sequence 12, Appl	c 925	19	1.6	75	2	US-08-776-944-13	Sequence 13, Appl
c 853	19	1.6	30	5	PCT-US95-10202-41	Sequence 41, Appl	c 926	19	1.6	76	4	US-09-244-794A-1	Sequence 1, Appl
c 854	19	1.6	30	5	PCT-US95-10203-41	Sequence 41, Appl	c 927	19	1.6	76	4	US-09-247-190-1	Sequence 1, Appl
c 855	19	1.6	30	5	PCT-US95-10220-41	Sequence 41, Appl	c 928	19	1.6	80	1	US-07-920-281C-25	Sequence 25, Appl
c 856	19	1.6	35	2	US-08-467-603-100	Sequence 100, App	c 929	19	1.6	80	4	US-08-466-277-25	Sequence 25, Appl
c 857	19	1.6	35	2	US-08-466-793-100	Sequence 100, App	c 930	19	1.6	83	1	US-08-120-827-100	Sequence 100, App
c 858	19	1.6	35	2	US-08-491-861A-100	Sequence 100, App	c 931	19	1.6	83	1	US-08-478-675-100	Sequence 100, App
c 859	19	1.6	37	1	US-08-113-646A-44	Sequence 44, Appl	c 932	19	1.6	88	1	US-07-750-080A-11	Sequence 11, Appl
c 860	19	1.6	40	1	US-08-433-505-10	Sequence 10, Appl	c 933	19	1.6	88	3	US-08-651-472-11	Sequence 11, Appl
c 861	19	1.6	40	3	US-08-870-730-10	Sequence 10, Appl	c 934	19	1.6	88	4	US-08-358-928-11	Sequence 11, Appl
c 862	19	1.6	40	4	US-09-306-290-2	Sequence 2, Appl	c 935	19	1.6	90	4	US-09-065-058-16	Sequence 16, Appl
c 863	19	1.6	40	4	US-09-306-290-5	Sequence 5, Appl	c 936	19	1.6	91	2	US-08-525-742-51	Sequence 51, Appl
c 864	19	1.6	40	4	US-09-306-290-9	Sequence 9, Appl	c 937	19	1.6	92	1	US-07-750-080A-12	Sequence 12, Appl
c 865	19	1.6	40	4	US-08-484-575A-11	Sequence 11, Appl	c 938	19	1.6	92	3	US-08-651-472-12	Sequence 12, Appl
c 866	19	1.6	42	2	US-08-477-459-11	Sequence 11, Appl	c 939	19	1.6	92	4	US-08-358-928-12	Sequence 12, Appl
c 867	19	1.6	42	3	US-08-479-869-11	Sequence 11, Appl	c 940	19	1.6	93	1	US-07-750-080A-40	Sequence 40, Appl
c 868	19	1.6	42	3	US-08-486-414-11	Sequence 11, Appl	c 941	19	1.6	93	2	US-08-525-742-28	Sequence 28, Appl
c 869	19	1.6	42	3	US-08-486-414-11	Sequence 11, Appl	c 942	19	1.6	93	3	US-08-651-472-40	Sequence 40, Appl
c 870	19	1.6	42	4	US-09-306-290-13	Sequence 13, Appl	c 943	19	1.6	93	4	US-08-358-928-40	Sequence 40, Appl
c 871	19	1.6	42	5	PCT-US94-01826A-11	Sequence 11, Appl	c 944	19	1.6	95	2	US-08-525-742-29	Sequence 29, Appl
c 872	19	1.6	42	5	PCT-US94-02252A-11	Sequence 11, Appl	c 945	19	1.6	96	2	US-08-525-742-30	Sequence 30, Appl
c 873	19	1.6	45	3	US-08-481-435-39	Sequence 39, Appl	c 946	19	1.6	97	1	US-07-750-080A-41	Sequence 41, Appl
c 874	19	1.6	45	3	US-08-481-435-40	Sequence 40, Appl	c 947	19	1.6	97	2	US-08-525-742-27	Sequence 27, Appl
c 875	19	1.6	46	1	US-08-232-463-40	Sequence 40, Appl	c 948	19	1.6	97	3	US-08-651-472-41	Sequence 41, Appl
c 876	19	1.6	46	4	US-08-990-823-108	Sequence 108, App	c 949	19	1.6	97	4	US-08-358-928-41	Sequence 41, Appl
c 877	19	1.6	46	5	PCT-US94-05407-3	Sequence 3, Appl	c 950	19	1.6	102	1	US-07-820-154A-10	Sequence 10, Appl
c 878	19	1.6	46	5	PCT-US94-05407-10	Sequence 10, Appl	c 951	19	1.6	102	2	US-08-097-554A-10	Sequence 10, Appl
c 879	19	1.6	48	1	US-08-380-438-6	Sequence 6, Appl	c 952	19	1.6	102	3	US-08-480-640A-10	Sequence 10, Appl
c 880	19	1.6	49	5	PCT-US96-07709-39	Sequence 39, Appl	c 953	19	1.6	102	3	US-08-295-802-10	Sequence 10, Appl
c 881	19	1.6	49	5	PCT-US96-07709-40	Sequence 40, Appl	c 954	19	1.6	102	4	US-08-686-968C-106	Sequence 106, App
c 882	19	1.6	49	5	PCT-US96-09848-19	Sequence 19, Appl	c 955	19	1.6	102	4	US-08-488-237A-10	Sequence 10, Appl
c 883	19	1.6	49	5	PCT-US96-09848-20	Sequence 20, Appl	c 956	19	1.6	102	5	PCT-US93-0032A-10	Sequence 10, Appl
c 884	19	1.6	50	2	US-08-663-823B-74	Sequence 74, Appl	c 957	19	1.6	108	1	US-07-820-154A-32	Sequence 32, Appl
c 885	19	1.6	52	2	US-08-467-603-59	Sequence 59, Appl	c 958	19	1.6	108	2	US-08-097-554A-32	Sequence 32, Appl
c 886	19	1.6	52	2	US-08-466-793-59	Sequence 59, Appl	c 959	19	1.6	108	3	US-08-480-640A-32	Sequence 32, Appl
c 887	19	1.6	52	2	US-08-776-944-7	Sequence 7, Appl	c 960	19	1.6	108	3	US-08-295-802-32	Sequence 32, Appl
c 888	19	1.6	52	2	US-08-491-861A-59	Sequence 59, Appl	c 961	19	1.6	108	4	US-08-488-237A-32	Sequence 32, Appl
c 889	19	1.6	54	2	US-08-418-848A-57	Sequence 57, Appl	c 962	19	1.6	108	5	PCT-US93-0032A-32	Sequence 32, Appl
c 890	19	1.6	55	1	US-07-803-633A-3	Sequence 3, Appl	c 963	19	1.6	111	2	US-08-097-554A-78	Sequence 78, Appl
c 891	19	1.6	55	1	US-07-803-633A-4	Sequence 4, Appl	c 964	19	1.6	111	4	US-08-991-789A-93	Sequence 93, Appl
c 892	19	1.6	55	1	US-07-750-080A-38	Sequence 38, Appl	c 965	19	1.6	111	4	US-08-991-789A-145	Sequence 145, App
c 893	19	1.6	55	1	US-07-750-080A-39	Sequence 39, Appl	c 966	19	1.6	113	4	US-08-943-731-80	Sequence 80, Appl
c 894	19	1.6	55	1	US-08-323-084A-18	Sequence 18, Appl	c 967	19	1.6	117	3	US-08-480-640A-78	Sequence 78, Appl
c 895	19	1.6	55	1	US-08-674-008-18	Sequence 18, Appl	c 968	19	1.6	117	3	US-08-295-802-78	Sequence 78, Appl
c 896	19	1.6	55	2	US-08-525-742-13	Sequence 13, Appl	c 969	19	1.6	117	4	US-08-686-968C-130	Sequence 130, App
c 897	19	1.6	55	2	US-08-525-742-14	Sequence 14, Appl	c 970	19	1.6	117	4	US-08-686-968C-144	Sequence 144, App
c 898	19	1.6	55	2	US-08-771-624B-8	Sequence 8, Appl	c 971	19	1.6	117	4	US-08-488-237A-78	Sequence 78, Appl
c 899	19	1.6	55	3	US-08-651-472-38	Sequence 38, Appl	c 972	19	1.6	119	2	US-08-097-554A-86	Sequence 86, Appl
c 900	19	1.6	55	3	US-08-651-472-39	Sequence 39, Appl	c 973	19	1.6	119	2	US-08-097-554A-95	Sequence 95, Appl
c 901	19	1.6	55	3	US-08-358-928-38	Sequence 38, Appl	c 974	19	1.6	120	4	US-08-686-968C-151	Sequence 151, App
c 902	19	1.6	55	4	US-08-358-928-39	Sequence 39, Appl	c 975	19	1.6	123	4	US-08-686-968C-140	Sequence 140, App
c 903	19	1.6	56	1	US-08-275-169-1	Sequence 1, Appl	c 976	19	1.6	123	4	US-09-007-005-1	Sequence 1, Appl

977 19 1.6 123 4 US-09-244-796-1
c 978 19 1.6 124 3 US-08-480-640A-86
c 979 19 1.6 124 3 US-08-480-640A-95
c 980 19 1.6 124 3 US-08-295-802-86
c 981 19 1.6 124 3 US-08-295-802-95
c 982 19 1.6 124 4 US-08-488-237A-86
c 983 19 1.6 124 4 US-08-488-237A-95
c 984 19 1.6 127 1 US-07-750-080A-13
c 985 19 1.6 127 3 US-08-480-640A-160
c 986 19 1.6 127 3 US-08-651-472-13
c 987 19 1.6 127 3 US-08-295-802-160
c 988 19 1.6 127 4 US-08-488-237A-160
c 989 19 1.6 127 4 US-08-358-928-13
c 990 19 1.6 128 3 US-08-480-640A-145
c 991 19 1.6 128 3 US-08-295-802-145
c 992 19 1.6 128 4 US-08-488-237A-145
c 993 19 1.6 129 1 US-08-664-449-38
c 994 19 1.6 130 6 5198345-15
c 995 19 1.6 130 6 5198345-15
c 996 19 1.6 133 3 US-08-480-640A-176
c 997 19 1.6 133 3 US-08-295-802-176
c 998 19 1.6 133 4 US-08-488-237A-176
c 999 19 1.6 134 1 US-07-750-080A-14
c1000 19 1.6 134 3 US-08-651-472-14

ALIGNMENTS

RESULT 1
US-08-924-747-1
; Sequence 1, Application US/08924747
; Patent No. 6063570
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEFE, DANIEL
; TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE
; TITLE OF INVENTION: ENZYMES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
; SOFTWARE: MICROSOFT WORD VERSION 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/924,747
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: CL-1108
; TELEPHONE: 302-892-8112
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 886 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: SFL27B04

US-08-924-747-1
Query Match 2.0%; Score 24; DB 3; Length 886;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1150 tatttcaaaaaaaaaaaaaa 1173
|||||
Db 863 TATTTCACAAAAA 886
RESULT 2
US-09-247-373B-1
; Sequence 1, Application US/09247373B
; Patent No. 6168954
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEFE, DANIEL
; TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
; FILE REFERENCE: CL-1108-A
; CURRENT APPLICATION NUMBER: US/09/247,373B
; CURRENT FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 08/924,747
; PRIOR FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 886
; TYPE: DNA
; ORGANISM: SOYBEAN
US-09-247-373B-1
Query Match 2.0%; Score 24; DB 4; Length 886;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1150 tatttcaaaaaaaaaaaaaa 1173
|||||
Db 863 tatttcaaaaaaaaaaaaaa 886
RESULT 3
US-09-296-715-1
; Sequence 1, Application US/09296715
; Patent No. 6171839
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEFE, DANIEL
; TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE
; TITLE OF INVENTION: ENZYMES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
; SOFTWARE: MICROSOFT WORD VERSION 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/296,715
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: CL-1108

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 886 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: SEI.27B04
; US-09-296-715-1

Query Match 2.0%; Score 24; DB 4; Length 886;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1150 tatttcaaaaaaaaaaaaaaa 1173
|||||

DB 863 TATTTCACAAAAA 886

RESULT 4

US-09-323-427-6
; Sequence 6, Application US/09323427
; Patent No. 6248329
; GENERAL INFORMATION:
; APPLICANT: Chandrashekar, Ramaswamy
; APPLICANT: Morales, Tony H.
; TITLE OF INVENTION: Parasitic Helminth Cuticlin Proteins, Nucleic Acid
; TITLE OF INVENTION: Molecules, and Uses Thereof
; FILE REFERENCE: HW-8
; CURRENT APPLICATION NUMBER: US/09/323,427
; CURRENT FILING DATE: 1999-06-01
; EARLIER APPLICATION NUMBER: 60/087,435
; EARLIER FILING DATE: 1998-06-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1372
; TYPE: DNA
; ORGANISM: Dirofilaria immitis
; US-09-323-427-6

Query Match 2.0%; Score 24; DB 4; Length 1372;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1150 tatttcaaaaaaaaaaaaaaa 1173
|||||

DB 1341 tatttcaaaaaaaaaaaaaaa 1364

RESULT 5

US-09-323-427-7/c
; Sequence 7, Application US/09323427
; Patent No. 6248329
; GENERAL INFORMATION:
; APPLICANT: Chandrashekar, Ramaswamy
; APPLICANT: Morales, Tony H.
; TITLE OF INVENTION: Parasitic Helminth Cuticlin Proteins, Nucleic Acid
; TITLE OF INVENTION: Molecules, and Uses Thereof
; FILE REFERENCE: HW-8
; CURRENT APPLICATION NUMBER: US/09/323,427
; CURRENT FILING DATE: 1999-06-01
; EARLIER APPLICATION NUMBER: 60/087,435
; EARLIER FILING DATE: 1998-06-01
; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1372
; TYPE: DNA
; ORGANISM: Dirofilaria immitis
; US-09-323-427-7

Query Match 2.0%; Score 24; DB 4; Length 1372;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1150 tatttcaaaaaaaaaaaaaaa 1173
|||||

DB 32 TATTTCACAAAAA 9

RESULT 6

US-08-175-158A-1
; Sequence 1, Application US/08175158A
; Patent No. 5986067
; GENERAL INFORMATION:
; APPLICANT: FUNK, Walter D.
; APPLICANT: MacGILLIVRAY, Ross T.A.
; APPLICANT: MASON, Anne B.
; APPLICANT: WOODWORTH, Robert C.
; TITLE OF INVENTION: RECOMBINANT TRANSFERRINS, TRANSFERRIN HALF-
; TITLE OF INVENTION: MOLECULES AND MUTANTS THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/175,158A
; FILING DATE: 28-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/832,029
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: UVI-005CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2327 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..2124
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 88..2124
; US-08-175-158A-1

Query Match 2.0%; Score 24; DB 2; Length 2327;
Best Local Similarity 100.0%; Pred. No. 0.47;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1150 tatttcaaaaaaaaaaaaaaa 1173
|||||
Db 2293 TATTTCACAAAAAAAAAAAAA 2316

RESULT 7

US-08-415-593-42
; Sequence 42, Application US/08415593
; Patent No. 5912140
; Patent No. 5912140 5776726
; GENERAL INFORMATION:
; APPLICANT: Whoriskey, Susan K.
; APPLICANT: Quinn, Cheryl L.
; APPLICANT: Tao, Nijun
; APPLICANT: Politis-Virk, Karen I.
; APPLICANT: Schimmel, Paul R.
; TITLE OF INVENTION: Recombinant Pneumocystis Aminoacyl tRNA
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,593
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CPI94-09
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-862-9540
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2993 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2934
US-08-415-593-42

Query Match 2.0%; Score 24; DB 2; Length 2993;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1150 tatttcaaaaaaaaaaaaaaa 1173
|||||
Db 2963 TATTTCACAAAAAAAAAAAAA 2986

RESULT 8

US-08-996-306-10/c
; Sequence 10, Application US/08996306
; Patent No. 5945522
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Chumakov, Ilya

; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Prostate cancer gene
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,306
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: GENSET.018A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: DNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PGRT32
; LOCATION: complement 5198..5221
; OTHER INFORMATION: Location relative to seqID3
US-08-996-306-10

Query Match 2.0%; Score 23; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1151 atttcaaaaaaaaaaaaaaa 1173
|||||
Db 24 ATTTCAAAAAAAAAAAAAA 2

RESULT 9

US-09-338-907-10/c
; Sequence 10, Application US/09338907
; Patent No. 6265546
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilya, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: PROSTATE CANCER GENE
; FILE REFERENCE: GENSET.18C1CP
; CURRENT APPLICATION NUMBER: US/09/338,907
; CURRENT FILING DATE: 1999-06-23
; EARLIER APPLICATION NUMBER: 08/996,306
; EARLIER FILING DATE: 1997-12-22
; EARLIER APPLICATION NUMBER: 60/099,658
; EARLIER FILING DATE: 1998-09-09
; EARLIER APPLICATION NUMBER: 09/218,207
; EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm

SEQ ID NO 10
LENGTH: 24
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..24
OTHER INFORMATION: primer oligonucleotide PGRT32
US-09-338-907-10

Query Match 2.0%; Score 23; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.9; Indels 0;
Matches 23; Conservative 0; Mismatches 0; Gaps 0;

Qy 1151 atttcaaaaaaaaaaaaaaaaa 1173
|||||
Db 24 ATTTCAAAAAAAAAAAAAAAAA 2

RESULT 10
US-08-741-881-3/c
Sequence 3, Application US/08741881
Patent No. 5789245
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/741,881
FILING DATE: 30-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-741-881-3

Query Match 2.0%; Score 23; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.8; Indels 0;
Matches 23; Conservative 0; Mismatches 0; Gaps 0;

Qy 1151 atttcaaaaaaaaaaaaaaaaa 1173
|||||
Db 41 ATTTCAAAAAAAAAAAAAAAAA 19

RESULT 11
US-08-739-158-3/c
Sequence 3, Application US/08739158
Patent No. 5814482
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/739,158
FILING DATE: 30-OCT-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-739-158-3

Query Match 2.0%; Score 23; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.8; Indels 0;
Matches 23; Conservative 0; Mismatches 0; Gaps 0;

Qy 1151 atttcaaaaaaaaaaaaaaaaa 1173
|||||
Db 41 ATTTCAAAAAAAAAAAAAAAAA 19

RESULT 12
US-08-739-167-3/c
Sequence 3, Application US/08739167
Patent No. 5843723
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington

COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 30-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-739-167-3

Query Match 2.0%; Score 23; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaaa 1173
|||||
DB 41 ATTTCAAAAAAAAAAAAAAAAA 19

RESULT 13
US-08-404-796-3/c
Sequence 3, Application US/08404796
Patent No. 6015686
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 15-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-404-796-3

Query Match 2.0%; Score 23; DB 3; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaaa 1173
|||||
DB 41 ATTTCAAAAAAAAAAAAAAAAA 19

RESULT 14
US-08-931-869-3/c
Sequence 3, Application US/08931869
Patent No. 6015694
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 16-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/404,796
FILING DATE: 15-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-931-869-3

Query Match 2.0%; Score 23; DB 3; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaaa 1173
|||||

Db 41 ATTTCAAAAAAAAAAAAAAAAAAAA 19

RESULT 15

US-08-741-881-21/c
; Sequence 21, Application US/08741881
; Patent No. 5789245
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,881
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-741-881-21

Query Match 2.0%; Score 23; DB 1; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1151 atttcaaaaaaaaaaaaaaaaaaa 1173
Db 41 ATTTCAAAAAAAAAAAAAAAAAAAA 19

RESULT 16

US-08-739-158-21/c
; Sequence 21, Application US/08739158
; Patent No. 5814482
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle

; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,158
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-739-158-21

Query Match 2.0%; Score 23; DB 1; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1151 atttcaaaaaaaaaaaaaaaaaaa 1173
Db 41 ATTTCAAAAAAAAAAAAAAAAAAAA 19

RESULT 17

US-08-739-167-21/c
; Sequence 21, Application US/08739167
; Patent No. 5843723
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,167
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-739-167-21

Query Match 2.0%; Score 23; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaa 1173
|||||
Db 41 ATTTCAAAAAAAAAAAAAAAAAA 19

RESULT 18
US-08-404-796-21/c
; Sequence 21, Application US/08404796
; Patent No. 6015686
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/404,796
; FILING DATE: 15-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 682-6031
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-404-796-21

Query Match 2.0%; Score 23; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaa 1173
|||||
Db 41 ATTTCAAAAAAAAAAAAAAAAAA 19

RESULT 19
US-08-931-869-21/c
; Sequence 21, Application US/08931869
; Patent No. 6015694
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/931,869
; FILING DATE: 16-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/404,796
; FILING DATE: 15-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-931-869-21

Query Match 2.0%; Score 23; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaa 1173
|||||
Db 41 ATTTCAAAAAAAAAAAAAAAAAA 19

RESULT 20
US-08-826-246-7
; Sequence 7, Application US/08826246
; Patent No. 6048709
; GENERAL INFORMATION:
; APPLICANT: Falb, Dean
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York

STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/826,246
FILING DATE: 28-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/799,910
FILING DATE: 13-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/011,787
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-078-999
TELEPHONE: (212)7909090
TELEFAX: (212)8699741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1036 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...546
OTHER INFORMATION:
US-08-826-246-7

Query Match 2.0%; Score 23; DB 3; Length 1036;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1150 tatttcaaaaaaaaaaaaaa 1172
|||||
DB 866 TATTCAAAAAAAAAAAAAA 888

RESULT 21
US-08-944-495-7
Sequence 7, Application US/08944495
Patent No. 6087477
GENERAL INFORMATION:
APPLICANT: Falb, Dean
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF
TITLE OF INVENTION: CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,495

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/799,910
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-067-999
TELEPHONE: (212)7909090
TELEFAX: (212)8699741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1036 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...546
OTHER INFORMATION:
US-08-944-495-7

Query Match 2.0%; Score 23; DB 3; Length 1036;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1150 tatttcaaaaaaaaaaaaaa 1172
|||||
DB 866 TATTCAAAAAAAAAAAAAA 888

RESULT 22
US-09-126-640-4
Sequence 4, Application US/09126640A
Patent No. 6099823
GENERAL INFORMATION:
APPLICANT: Falb, Dean A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
FILE REFERENCE: 7853-126
CURRENT APPLICATION NUMBER: US/09/126,640A
CURRENT FILING DATE: 1998-07-30
EARLIER APPLICATION NUMBER: 08/870,434
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 08/799,910
EARLIER FILING DATE: 1997-02-13
EARLIER APPLICATION NUMBER: 60/011,787
EARLIER FILING DATE: 1996-02-16
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 1036
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1036)
OTHER INFORMATION: n = A,T,C or G
US-09-126-640-4

Query Match 2.0%; Score 23; DB 3; Length 1036;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1150 tatttcaaaaaaaaaaaaaa 1172
|||||
DB 866 tatttcaaaaaaaaaaaaaa 888

; APPLICANT: ROSSMANN, JEAN
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES CODING FOR DEBRANCHING ENZYMES
 ; TITLE OF INVENTION: FROM POTATO
 ; FILE REFERENCE: GFB8


```
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaa 1173
    |||||
Db 2309 ATTTCAAAAAAAAAAAAAAAAA 2331

RESULT 26
US-08-765-243-1
; Sequence 1, Application US/08765243
; Patent No. 5935578
; GENERAL INFORMATION:
; APPLICANT: ALVES, KENNETH
; APPLICANT: GUPTA, SUNIL K.
; APPLICANT: HOLLIS, GREGORY F.
; TITLE OF INVENTION: CONTRACEPTIVE VACCINE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MARY A. APPOLLINA
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08765,243
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: APPOLLINA, MARY A
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19244Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2373 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-765-243-1

Query Match 2.0%; Score 23; DB 2; Length 2373;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaa 1173
    |||||
Db 2309 ATTTCAAAAAAAAAAAAAAAAA 2331

RESULT 27
PCT-US95-07295-1
; Sequence 1, Application PC/TUS9507295
; GENERAL INFORMATION:
; APPLICANT: ALVES, KENNETH
; APPLICANT: GUPTA, SUNIL K.
; APPLICANT: HOLLIS, GREGORY F.
; TITLE OF INVENTION: CONTRACEPTIVE VACCINE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MARY A. APPOLLINA
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,218
; FILING DATE: 14-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 008358-0004-999
```

```
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07295
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: APPOLLINA, MARY A
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19244Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2373 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
PCT-US95-07295-1

Query Match 2.0%; Score 23; DB 5; Length 2373;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaa 1173
    |||||
Db 2309 ATTTCAAAAAAAAAAAAAAAAA 2331

RESULT 28
US-08-972-218-2
; Sequence 2, Application US/08972218
; Patent No. 6197502
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Orberger, Georg H.
; APPLICANT: Koller, Daniel
; APPLICANT: Bailey, James E.
; TITLE OF INVENTION: EXPRESSION CLONING PROCESSES FOR THE
; TITLE OF INVENTION: DISCOVERY, CHARACTERIZATION AND ISOLATION OF GENES
; TITLE OF INVENTION: ENCODING POLYPEPTIDES WITH A PREDETERMINED PROPERTY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,218
; FILING DATE: 14-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 008358-0004-999
```

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 9521 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-972-218-2

Query Match 2.0%; Score 23; DB 4; Length 9521;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1151 atttcaaaaaaaaaaaaaaaaa 1173
|||||
Db 7123 ATTTCAAAAAAAAAAAAAAAAA 7145

RESULT 29
US-08-972-218-1
; Sequence 1, Application US/08972218
; Patent No. 6197502
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Orberger, Georg H.
; APPLICANT: Koller, Daniel
; APPLICANT: Bailey, James E.
; TITLE OF INVENTION: EXPRESSION CLONING PROCESSES FOR THE
; TITLE OF INVENTION: DISCOVERY, CHARACTERIZATION AND ISOLATION OF GENES
; TITLE OF INVENTION: ENCODING POLYPEPTIDES WITH A PREDETERMINED PROPERTY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of The Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,218
; FILING DATE: 14-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 008358-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13905 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-972-218-1

Query Match 2.0%; Score 23; DB 4; Length 13905;
Best Local Similarity 100.0%; Pred. No. 0.95;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1151 atttcaaaaaaaaaaaaaaaaa 1173
|||||
Db 11666 ATTTCAAAAAAAAAAAAAAAAA 11988

RESULT 30
US-08-741-881-1
; Sequence 1, Application US/08741881
; Patent No. 5789245
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,881
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16656 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-741-881-1

Query Match 2.0%; Score 23; DB 1; Length 16656;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1151 atttcaaaaaaaaaaaaaaaaa 1173
|||||
Db 11696 ATTTCAAAAAAAAAAAAAAAAA 11718

RESULT 31
US-08-739-158-1
; Sequence 1, Application US/08739158
; Patent No. 5814482
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,158
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16656 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-739-158-1

Query Match 2.0%; Score 23; DB 1; Length 16656;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1151 atttcaaaaaaaaaaaaaaa 1173
|||||
Db 11696 ATTTCAAAAAAAAAAAAA 11718

RESULT 32
US-08-739-167-1
; Sequence 1, Application US/08739167
; Patent No. 5843723
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,167
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.

; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16656 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-739-167-1

Query Match 2.0%; Score 23; DB 2; Length 16656;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1151 atttcaaaaaaaaaaaaaaa 1173
|||||
Db 11696 ATTTCAAAAAAAAAAAAA 11718

RESULT 33
US-08-404-796-1
; Sequence 1, Application US/08404796
; Patent No. 6015686
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/404,796
; FILING DATE: 15-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16656 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-404-796-1

Query Match 2.0%; Score 23; DB 3; Length 16656;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaa 1173
 |||
 Db 11696 ATTTCAAAAAAAAAAAAAAAAA 11718

RESULT 34

US-08-931-869-1
 ; Sequence 1, Application US/08931869
 ; Patent No. 6015694
 ; GENERAL INFORMATION:
 ; APPLICANT: Dubensky Jr, Thomas W
 ; APPLICANT: Polo, John M.
 ; APPLICANT: Ibanez, Carlos E.
 ; APPLICANT: Chang, Stephen M.W.
 ; APPLICANT: Jolly, Douglas J.
 ; APPLICANT: Driver, David A.
 ; APPLICANT: Belli, Barbara A.
 ; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
 ; NUMBER OF SEQUENCES: 128
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SEED and BERRY LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: US
 ; ZIP: 98104-7092
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/931,869
 ; FILING DATE: 16-SEP-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/404,796
 ; FILING DATE: 15-MAR-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McMasters, David D.
 ; REGISTRATION NUMBER: 33,963
 ; REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 16656 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-931-869-1

Query Match 2.0%; Score 23; DB 3; Length 16656;
 Best Local Similarity 100.0%; Pred. No. 0.93;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaa 1173
 |||
 Db 11696 ATTTCAAAAAAAAAAAAAAAAA 11718

RESULT 35

US-09-128-155-16/c
 ; Sequence 16, Application US/09128155
 ; Patent No. 6117654
 ; GENERAL INFORMATION:
 ; APPLICANT: Pan, Yang
 ; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
 ; TITLE OF INVENTION: AND USES THEREOF
 ; FILE REFERENCE: 09404/052001
 ; CURRENT APPLICATION NUMBER: US/09/128,155

; CURRENT FILING DATE: 1998-08-03
 ; EARLIER APPLICATION NUMBER: US 60/091,650
 ; EARLIER FILING DATE: 1998-07-02
 ; EARLIER APPLICATION NUMBER: US 60/054,646
 ; EARLIER FILING DATE: 1997-08-04
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 16
 ; LENGTH: 152331
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(152331)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-128-155-16

Query Match 2.0%; Score 23; DB 3; Length 152331;
 Best Local Similarity 100.0%; Pred. No. 0.73;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaa 1173
 |||
 Db 61197 ATTTCAAAAAAAAAAAAAAAAA 61175

RESULT 36

US-08-724-394A-20
 ; Sequence 20, Application US/08724394A
 ; Patent No. 5872237
 ; GENERAL INFORMATION:
 ; APPLICANT: Feder, John N.
 ; APPLICANT: Kronmal, Gregory S.
 ; APPLICANT: Lauer, Peter M.
 ; APPLICANT: Ruddy, David A.
 ; APPLICANT: Thomas, Winston
 ; APPLICANT: Tsuchihashi, Zenta
 ; APPLICANT: Wolff, Roger K.
 ; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
 ; STREET: Two Embarcadero Center, 8th Floor
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/724,394A
 ; FILING DATE: 01-OCT-1996
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fitts, Renee A.
 ; REGISTRATION NUMBER: 35,136
 ; REFERENCE/DOCKET NUMBER: 017957-000100
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-576-0200
 ; TELEFAX: 415-576-0300
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 246240 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: not relevant
 ; MOLECULE TYPE: cdna
 ; FEATURE:

NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-20

Query Match 2.0%; Score 23; DB 2; Length 246240;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaa 1173
|||||

DB 141094 ATTTCAAAAAAAAAAAAAAAAA 141116

RESULT 37

US-08-724-394A-21
Sequence 21, Application US/08724394A
Patent No. 5872237

GENERAL INFORMATION:

APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.

TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
TITLE OF INVENTION: Sequences and Antibodies Thereto

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/724,394A

FILING DATE: 01-OCT-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Fitts, Renee A.

REGISTRATION NUMBER: 35,136

REFERENCE/DOCKET NUMBER: 017957-000100

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 246240 base pairs

TYPE: nucleic acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: misc_feature

LOCATION: 1..246240

OTHER INFORMATION: /note= "HLA-H.CONTIG"

US-08-724-394A-21

Query Match 2.0%; Score 23; DB 2; Length 246240;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaa 1173
|||||

DB 141094 ATTTCAAAAAAAAAAAAAAAAA 141116

RESULT 38

US-08-724-394A-22

Sequence 22, Application US/08724394A

Patent No. 5872237

GENERAL INFORMATION:

APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.

TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el

TITLE OF INVENTION: Sequences and Antibodies Thereto

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/724,394A

FILING DATE: 01-OCT-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Fitts, Renee A.

REGISTRATION NUMBER: 35,136

REFERENCE/DOCKET NUMBER: 017957-000100

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 246240 base pairs

TYPE: nucleic acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: misc_feature

LOCATION: 1..246240

OTHER INFORMATION: /note= "HLA-H.CONTIG"

US-08-724-394A-22

Query Match 2.0%; Score 23; DB 2; Length 246240;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaa 1173
|||||

DB 141094 ATTTCAAAAAAAAAAAAAAAAA 141116

RESULT 39

US-09-306-290-21/c

Sequence 21, Application US/09306290

Patent No. 6221635

GENERAL INFORMATION:

APPLICANT: Rovera, Giovanni

APPLICANT: Mukhopadhyay, Sunil

TITLE OF INVENTION: METHODS FOR SOLID-PHASE AMPLIFICATION OF DNA TEMPLATE

TITLE OF INVENTION: (SPADT) USING MULTARRAYS

; FILE REFERENCE: 09924-10
; CURRENT APPLICATION NUMBER: US/09/306,290
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer p41
; OTHER INFORMATION: FH92
US-09-306-290-21

Query Match 1.9%; Score 22; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1152 ttccaaaaaa 1173
Db 25 TTTCAAAAAA 4

RESULT 40
US-08-991-840A-13/c
; Sequence 13, Application US/08991840A
; Patent No. 6261570
; GENERAL INFORMATION:
; APPLICANT: Michael D. Parker
; APPLICANT: Jonathan F. Smith
; APPLICANT: Bruce Crise
; APPLICANT: Mark Steve Oberste
; APPLICANT: Shannon Schmura
; TITLE OF INVENTION: Live Attenuated Virus Vaccines for Eastern Equine Encephalitis
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: USA MRMC - MRMC-JA
; CITY: FORT DETRICK, FREDERICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,840A
; FILING DATE: December 16, 1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: Provisional Application 60/047162,
; FILING DATE: May 20, 1997
; APPLICATION NUMBER: Provisional Application 60/053,652
; FILING DATE: July 24, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: 003/058/SAP RIID 96-01
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-5034
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 base pairs
; TYPE: Nucleic acid
; STRANDEDNESS: Double
; TOPOLOGY: Unknown
US-08-991-840A-13

Query Match 1.9%; Score 22; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1151 attcaaaaaa 1172
Db 34 ATTCAAAAAA 13

RESULT 41
US-08-482-182-70
; Sequence 70, Application US/08482182
; Patent No. 5861273
; GENERAL INFORMATION:
; APPLICANT: MASCARENHAS, DESMOND
; APPLICANT: OLSON, PAMELA S.
; TITLE OF INVENTION: CHROMOSOMAL EXPRESSION OF HETEROLOGOUS
; TITLE OF INVENTION: GENES IN BACTERIAL CELLS
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,182
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PARK, FREDDIE K.
; REGISTRATION NUMBER: 35,636
; REFERENCE/DOCKET NUMBER: 22095-20281.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 79 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-482-182-70

Query Match 1.9%; Score 22; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 584 gcaccaccaccaccacgac 605
Db 31 GCACCACCACCACCACGAC 52

RESULT 42
US-08-747-121-2
; Sequence 2, Application US/08747121
; Patent No. 5874290
; GENERAL INFORMATION:
; APPLICANT: Murphy, Gerald
; APPLICANT: Boynton, Alton
; APPLICANT: Sehgal, Anil
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID
; TITLE OF INVENTION: SEQUENCES OF A D2-2 GENE ASSOCIATED WITH
; TITLE OF INVENTION: BRAIN TUMORS AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/747,121
 ; FILING DATE: 08-NOV-1996
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Baldwin, Geraldine F
 ; REGISTRATION NUMBER: 31,232
 ; REFERENCE/DOCKET NUMBER: 8511-008
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212)7909090
 ; TELEFAX: (212)8698864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 144 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-747-121-2

Query Match 1.9%; Score 22; DB 2; Length 144;
 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1152 ttccaaaaaa 1173
 Db 122 TTTCAAAAAA 143

RESULT 43
 US-09-385-982-387/c
 ; Sequence 387, Application US/09385982
 ; Patent No. 6262334
 ; GENERAL INFORMATION:
 ; APPLICANT: ENDEGE, WILSON O., ET AL.
 ; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
 ; TITLE OF INVENTION: PRODUCTS: II
 ; FILE REFERENCE: CCDNA-260XX
 ; CURRENT APPLICATION NUMBER: US/09/385,982
 ; CURRENT FILING DATE: 1999-08-30
 ; EARLIER APPLICATION NUMBER: 09/328,111
 ; EARLIER FILING DATE: 1999-06-08
 ; EARLIER APPLICATION NUMBER: 60/117,393
 ; EARLIER FILING DATE: 1999-01-27
 ; EARLIER APPLICATION NUMBER: 60/098,639
 ; EARLIER FILING DATE: 1998-08-31
 ; NUMBER OF SEQ ID NOS: 544
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 387
 ; LENGTH: 256
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-385-982-387

Query Match 1.9%; Score 22; DB 4; Length 256;
 Best Local Similarity 100.0%; Pred. No. 3.6;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1152 ttccaaaaaa 1173
 Db 35 TTTCAAAAAA 14

RESULT 44
 US-09-385-982-508
 ; Sequence 508, Application US/09385982
 ; Patent No. 6262334
 ; GENERAL INFORMATION:
 ; APPLICANT: ENDEGE, WILSON O., ET AL.
 ; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
 ; TITLE OF INVENTION: PRODUCTS: II
 ; FILE REFERENCE: CCDNA-260XX
 ; CURRENT APPLICATION NUMBER: US/09/385,982
 ; CURRENT FILING DATE: 1999-08-30
 ; EARLIER APPLICATION NUMBER: 09/328,111
 ; EARLIER FILING DATE: 1999-06-08
 ; EARLIER APPLICATION NUMBER: 60/117,393
 ; EARLIER FILING DATE: 1999-01-27
 ; EARLIER APPLICATION NUMBER: 60/098,639
 ; EARLIER FILING DATE: 1998-08-31
 ; NUMBER OF SEQ ID NOS: 544
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 508
 ; LENGTH: 336
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(336)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-385-982-508

Query Match 1.9%; Score 22; DB 4; Length 336;
 Best Local Similarity 100.0%; Pred. No. 3.5;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1152 ttccaaaaaa 1173
 Db 309 ttccaaaaaa 330

RESULT 45
 US-09-385-982-203/c
 ; Sequence 203, Application US/09385982
 ; Patent No. 6262334
 ; GENERAL INFORMATION:
 ; APPLICANT: ENDEGE, WILSON O., ET AL.
 ; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
 ; TITLE OF INVENTION: PRODUCTS: II
 ; FILE REFERENCE: CCDNA-260XX
 ; CURRENT APPLICATION NUMBER: US/09/385,982
 ; CURRENT FILING DATE: 1999-08-30
 ; EARLIER APPLICATION NUMBER: 09/328,111
 ; EARLIER FILING DATE: 1999-06-08
 ; EARLIER APPLICATION NUMBER: 60/117,393
 ; EARLIER FILING DATE: 1999-01-27
 ; EARLIER APPLICATION NUMBER: 60/098,639
 ; EARLIER FILING DATE: 1998-08-31
 ; NUMBER OF SEQ ID NOS: 544
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 203
 ; LENGTH: 577
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(577)
 ; OTHER INFORMATION: n = A,T,C or G

APPL. TO

NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.422C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 581 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-993-674A-22

Query Match 1.9%; Score 22; DB 4; Length 581;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1152 ttccaataaaataaaataaa 1173
|||||
DB 541 TTCAAAAAAATAAAAAA 562

RESULT 49

US-09-091-590A-2
Sequence 2, Application US/09091590A
Patent No. 6242574
GENERAL INFORMATION:
APPLICANT: Nielsen, Klaus
APPLICANT: Kroll Kristensen, Anne
APPLICANT: Brunstedt, Janne
TITLE OF INVENTION: Anti-Microbial Proteins
FILE REFERENCE: S-137-1101/MA/A/SGS/PCT
CURRENT APPLICATION NUMBER: US/09/091,590A
CURRENT FILING DATE: 1999-05-06
PRIOR APPLICATION NUMBER: PCT/JEP96/05765
PRIOR FILING DATE: 1996-12-20
PRIOR APPLICATION NUMBER: GB 9526238.2
PRIOR FILING DATE: 1995-12-21
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 587
TYPE: DNA
ORGANISM: Beta vulgaris
FEATURE:
NAME/KEY: CDS
LOCATION: (129)..(374)
US-09-091-590A-2

Query Match 1.9%; Score 22; DB 4; Length 587;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1152 ttccaataaaataaaataaa 1173
|||||
DB 566 ttccaataaaataaaataaa 587

RESULT 50

US-09-385-982-265/c
Sequence 265, Application US/09385982
Patent No. 6262334
GENERAL INFORMATION:
APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS: II
FILE REFERENCE: CCDNA-260XX
CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: 09/328,111

EARLIER FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 60/098,639
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 544
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 265
LENGTH: 592
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(592)
OTHER INFORMATION: n = A,T,C or G
US-09-385-982-265

Query Match 1.9%; Score 22; DB 4; Length 592;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1152 ttccaataaaataaaataaa 1173
|||||
DB 36 TTCAAAAAAATAAAAAA 15

Search completed: December 27, 2001, 15:00:45
Job time: 697 sec

